

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LSRKAVSDMLTACKQASFHPDVSDEVTRALRF GTECTLGYLDLLEHVLVILQKPTPELKQQLAAFS KRVAGAVTELIQAAEAMKGTWVDPEDPTVIAE TELLGAAASIEAAKKLEQLKPRAPKQADETL DFEEQILEAAKSIAAATSALVKSASAAQRELVAQ GKVGSIPANAADDGQWSQGLISAARMVAAATSS LCEAANASVQGHASEEKLISAKQVAASTAQLL VACKVKADQDSEAMRRLQAAGNAVKRASDNL VRAAQKAAFGKADDDDVVVKTKFVGGAQIIAA QEEMLKKEERELEEARKKLAQIRQQQYKFLPTL REDEG
3441	A	3	1584	NSARGGVGVRGARAMATVQEKAALNLSALHS PAHRPPGFSVAQKPFATYVWSSIINTLQTQVEV KKRRHRLKRHNDCFVGSEAVDVIFSHLIQNKYF GDVDIPRAKVVRVCQALMDYKVFVPTKVF KDKKPTFEDSSCSLYRFTTIPNQDSQLGKENKLY SPARYADALFKSSDIRSLEDLWENLSLKPANS PHVNISTLSPQVINEVWQEETIGRLLQLVDLPLL DSLLKQGEAVPKIPQKRQSTMVNSSNYLDRGIL KAYSQDEDEWLSAIDCLEYLPDQMVVEISRSF PEQPDRTDLVKELLFDAIGRYSSREPLLNHLS VHNGIAELLVNGKTEIALEATQLLLKLLDFQNR EFRLLYFMAVAANPSEFKLQKESDNRMVVKRI FSKAIVDNKNLSKGKTDLLVLFLMDHQKDVFKI PGTLHKIVSVKILMAIQNGRDPNRDAGYTCQRI DQRDYSNITEKTTIDELLYLLKTLDEDSKLSAKE KKKLLGQFYKCHPDIFIEHFGD
3442	A	160	822	SPASGHCLRLNGAAMFGLVAGRLVQTAAQQ VAEDKFVFDLPDYESINHVVFMLGTIPFPEGMG GSVYFSYPDSNGMPVWQLLGFVTNGKPSAIFKIS GLKSGEGSQHPFGAMNIVRTPSVAQIGISVELLDS MAQQTPVGNAAVSSVDSFTQFTQKMLDNFYNF ASSFAVSQ/VPDDTQ/RPSEMFIPANVVLKWEYENF QRRSTEPSLLENIIWIKINF
3443	A	3	1373	SWHVRRLWLEATMAGGMKVAVSPA VGP GPWG SGVGGGTVRLLILSGCLVYGTAETDVNVVML QESQVCEKRASQQFCYTNVLIPQWHDWTRIQIR VNSSRLVRVTQVENEEKLKELEQFSIWNFFSSFL KEKLN DTYVNVGLYSTKTCLKVEIEKDTKYSVI VIRRFDPKFLVFLGLMLFFCGDLLSRSQIFYYS TGMTVGIVASLALIIIFILSKFMPPKSPYVILVGGW SFSLYLIQLVFKNLQEIWRWCYQYLLSYLTVGFM MSFAVCYKYGPLENERSINLLTWLQLMGLCFM YSGIQIPHIALAIIIALCTKNLEHPQWL YITCRKV CKGAEKVPVPRLLTEEEYRIQGEVETRKALEELR EFCNSPDCSAWKTVSRIQSPKRFADFVEGSSHLT PNEVSVHEQEYGLGSIIAQDEIYEEASSEEDSYS RCPAITQNNFLT
3444	A	566	1718	KGLERTCCAMEESDSEKTTEKENLGPRMDPLG EPGAGSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIVFDVESR ELEKDMHYQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DETL YKAWSSIVYQLIPNVQQLEMNLRNFAEIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMVRNSNFAAFIDIFTSN TYVMVMSDPSIPSAATLINIRNARKHFEKLERV DGPQKQCLLMR
3445	A	566	1718	KGLERTCCAMEESDSEKTEKENLGPRMDPPLG EPG\GSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRIHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESR ELEKDMHYQQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW DETL YKAWSSIVYQLIPNVQQLEMNLRNFAEIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMVRNSNFAAFIDIFTSN TYVMVMSDPSIPSAATLINIRNARKHFEKLERV DGPQKQCLLMR
3446	A	566	1718	KGLERTCCAMEESDSEKTEKENLGPRMDPPLG EPG\GSLGWVLPNTAMKKKVLLMGKSGSGKTS MRSIIFANYIARDTRRLGATILDRIHSLQINSSLST YSLVDSVGNTKTFDVEHSHVRLGNLVLNLWDC GGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESR ELEKDMHYQQSCLEAILQNSPDAKIFCLVHKMD LVQEDQRDLIFKEREEDLRRLSRPLECSCFRTSIW DETL YKAWSSIVYQLIPNVQQLEMNLRNFAEIE ADEVLLFERATFLVISHYQCKEQRDAHRFEKISNI IKQFKLSCSKLAASFQSMVRNSNFAAFIDIFTSN TYVMVMSDPSIPSAATLINIRNARKHFEKLERV DGPQKQCLLMR
3447	A	1	2930	VLLGPLWDKLSTADHPVIVTMASKRKSTTPCMIP VKTVVLQDASMEAQPAETLPEGPQQDLPEASA ASSEAAQNPSSTDGSTLANGHRSTLDGYLYSCK YCDFRSHDMTQFVGHMNSEHTDFNKDPTFVCSG CSFLAKTPEGLSLHNATCHSGEASFVWNVAKPD NHVVVEQSIPESTSTPDLAGEPSAEGADGQAEIIT KTPIMKIMKGKAEAKKIHTLKENVPSQPVGEALP KLSTGEMEVREGDHSFINGAVPVRQASASSAKN PHAANGPLIGTVPVLPAGIAQFLSLQQQPPVHAQ HHVHQPLPTAKALPKVMIPLSSIPTYSAAAMDSNS FLKNSFHKFPYPTKAELCYLTVVTKYPEEQLKIW FTAQRLKQGISWSPEEIEDARKKMFNTVIQSVPO PTITVLNTPLVASAGNVQHLLQAALPGHVVGQPE GTGGGLLVTPQLMANGLATSSPLPLTVTSVPK QPGVAPINTVCSNTTSAVKVVNAAQSLLTACPSI TSQAFLDASIYKNKKSHEQLSALKGSFCRNQFPG QSEVEHLTKVTGLSTREVRKWFSDRRYHCRNLK GSRAMIPGDHRSIHDSVPEVSFSPSSKVPEVTCIPT TATLATHPSAKRQSWHQTPDFTPTKYKERAPEQ LRALESSFAQNPLPLDEELDRLRSETKMTREIDS WFSERRKKVNAEETKKAENASQEEEEAAEDEG GEEDLASELRVSGENGSLPSSHILAERKVSPIK INLKNLRVTEANGRNEIPGLGACDPEDDESINKLA EQLPGKVSCKKTAAQQRHLLRQLFVQTQWPSNQD YDSIMAQTGLPRPEVVRWFGDSRYALKNGQLK WYEDYKRGNFPPGLLVIAAPGNRELLQDYMYMTHK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				MLYEEDLQNLCDKTMSSQQVKQWFAEKMGEETRAVADTGSEDQGPQTGELTAVHKMGMDTYSEVSENSESWEPRVPEASSEPFDTSSPQAGRQLETD
3448	A	2	1324	FVARAEKGFRRTREAHLLQVAGVGTGLQNGASLSGLASGVMAQRAFPNPYADYNKSLAEGYFDAAGRLTPEFSQRLTNKIRELLQQMERGLKSADPRDGTGYTGWAGIAVLYLHLYDVFGDPAYLQLAHGYVKQSLNCLTKRSITFLCGDAGPLAVA AVLHYHKMNEKQAEDCITRLIHLNKIDPHAPNEMLYGRIGYIYALLFVNKNFGVEKIPQSHIQICETILTSGENLARKRNF TAKSPLMYEWEYQEYYVGAAGLAGIYIYLMQPSLQVSQGLHSLVKPSVDYVCQLKFPSGNYPPCIGDNRDLLVHWCHGAPGVIMLIQAYKVF/REREKYLCDAYQCADVWQYGLLKKGYGLCY/GSAGNAY AFLTYNLTDQDMKYLYRACKFAEWCLEYGEHGCRTPDTPFSLFEGMAGTIYFLADLLFTKAR/FPAFEL
3449	A	3	2389	SRHVTGAARSPSRAGPSDPPAMGDEDDDESCAVELRITEANLTGHEEKVSVENFELLKVLGTGAYGKVFLVRKAGGHDAGKLYAMKVLKAAALVQRAKTQEHTRTERSVLELVRQAPFLVTLHYAFQTDAKLHLILDYVSGGEMFTHLYQRQYFKEAEVRVYGGEIVLALHLHLKLGIIYRDLKLENVLLDSEGHIVLTD FGLSKEFLTEEKERTFSFCGTIEYMAPEIIRSKTGHGKAVDWWSLGILLFELLTGASPF TLEGERNTQAEVSRRLKCSPPFPFRIGPVAQDLLQRL LCKDPKKRLGAGPQGAQEVRNHPFFQGLDWVALAARKIPAPFRPQIRSELDVGWFAEEFTRLEPVYSPPGQPPPGDPRIQGYSFVAP SILFDHNNAVMTDGLEAPGAGDRPGRAAVARSAMMQDSPFFQYELDLREPALGQGSFVCRRCRQRQSGQEF AVKILSRRL EANTQREVAALRLCQSHPNVNLHEVHHDQLHTYLVLEL LRGELLEHIRKKRHFSESEASQILRSLVSAVSFMHEEAGVVHRDLKPENILYADDTGPAPVKIIDFG/FSRRLRPQSPGVPMQTPSFTLQYAAPELLAQGYDESCDLWSLGVILYMMLSGQAPFQGASGQGGQSQA AEIMCKIREGRFSLDGEAWQGVSEEAKELVRGLLTVDPAKRLKLEGLRGSSWLQDGSARSSPPLRTPDVLESSGPAVRSGLNATFMAFNRGKREGFFLKSVENAPLAKRRKQKLRSATASRRGSPAPANPGRAPVASKGAPRRANGPLPPS
3450	A	201	1705	KGTEMNKSRRWQSRRRHGRRSHQQNPWFRLRDS EDRSDSRAA QPAHDSGHGDDESPSTSSGTAGTSSVP ELPGFYFDPEKKRYFRLLPGHNNCNPLTKESIRQKEMESKRLRL LQEEDRRKKIARMGFNASSMLRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSM DPSALASDRFNILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTP TLKVFMHENLYFTNRKVNSVCWASLNHLDSHILLCLMGLAETPGCATLLPASLFVNSHPAGIDRPGWMLCSFRIPGAWSCAWSLNIQANNCFSTGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNCGCRSGEIFAIDLRCGNQKGWKATRLFHDSAVTSVRILQDEQYLMASDMAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVGQDCYTRIWSLHDARLLRTIPSPYPASKAD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3451	A	19	6033	<p>IPSVAFSSRLGGSRGAPGLLMAVGQDLYCYSYS</p> <p>LLSAML SHGAGLALWITLSLLQTGLAEPERCNFT</p> <p>LAESKASSHSVSIQWRILGSPCNFSLIYSSDTLGA</p> <p>ALCPTFRIDNTTYGCNLQDLQAGTIYNFKIISLDE</p> <p>ERTVVLQTDPLPPARFGVSKEKTTSTGLHVWWT</p> <p>PSSGKVTSYEVQLFDENNQKIQGVQIQESTSWNE</p> <p>YTFFNLTAGSKYNIAITAVSGGKRSFSVYTNGST</p> <p>VPSPVKDIGISTKANSLISWSHGSGNVERYRLM</p> <p>LMDKGILVHGGVVDKHATSYAFHGLSPGYLYNL</p> <p>TVMTEAAGLQNYRWKLVRTAPMEVSNLKVNTD</p> <p>GSLSLKVKWQRPQG\NVDSYNITLSHGKTIKESR</p> <p>VLAPWITETHFKELVPGRLY\QVTCSAVSLGELS</p> <p>AQKMAVGRTFDPKVANLEANNGRMRSLVVS</p> <p>WSPPAGDWEQYRILLFNDSSVLLNITVGKEETQ</p> <p>YVMDGTGLVPGRQYEVVIVESGNLKNSERCQG</p> <p>RTVPLAVLQLRVKHANETSLSIMWQTPVAEWEK</p> <p>YIISLADRDLILLHKSLSKDAKEFTFDLVPGRKY</p> <p>MATVTSISGDLKNSSSVKGRTVPAQVTDLHVAN</p> <p>QGM TSSLFTNWTQAQGDVEFYQVLLIHENVVIK</p> <p>NESISSETSRYSFHSLSGSLYSVVVTTVSGGISSR</p> <p>QVVVEGRTVPSSVSGVTVNNSGRNDYLSVSWLL</p> <p>APGDVDNYEVTLSHDGKVVQSLVIKSVRECSF</p> <p>SSLTPGRLYTVTITTRSGKYENHSFSQERTVPDKV</p> <p>QGVSVSNSARSDYLRVSWVHATGDFDHYEVTIK</p> <p>NKNNFIQTKSIPKSENECVFVQLVPGRLYSVTVT</p> <p>TKSGQYEANEQNGRTIPEPVKDLTLRNRSTEDL</p> <p>HVTWSGANGDVDQYEQILLFNDMKVFPFHLVN</p> <p>TATEYRFTSLTPGRQYKILVLTISGDVQSAFIEG</p> <p>FTVPSA VKNIHISPNGATDSLTVNWTGGGDVDS</p> <p>YTVSAFRHSQKVDSQTIPKHVFEHTFHRLEAGEQ</p> <p>YQIMIASVSGSLKNQINVVGRTPASVQGVADN</p> <p>AYSSYSLIVSWQKAAGVAERYDILLTENGILLR</p> <p>NTSEPATTKQHKFEDLTPGKKYKIQILTVSGGLFS</p> <p>KEAQTEGRTVPAAVTDLRITENSTRHLSFRWTAS</p> <p>EGELSWYNIFLYNPDGNLQERAQVDPLVQSFSFQ</p> <p>NLLQGRMYKMOVIVTHSGELSNESFIFGRTPASV</p> <p>SHLRGSNRNTTDSLWFWNSPASGDFDYELILYN</p> <p>PNGTKKENWKDKDLTEWRFQGLVPGRKYVYLW</p> <p>VVTHSGDLSNKVTAESRTAPSPPSLMSFIADANT</p> <p>SLAITWKGPPDWDYNDFELQWLPRDALTVFNP</p> <p>YNNRKSEGRIVYGLRPGRSYQFNVKTVSGDSWK</p> <p>TYSKPIFGSVRTKPKIQNLHCRPQNSTALACSWI</p> <p>PPDSDFDGY SIECRKMDTQEVFESRKLEKEKSL</p> <p>NIMMLVPHKRYLVSIKVQSAGMTSEVVEDSTIT</p> <p>MIDRPPPPPPHIRVNEKDVLSKSSINFVNCSWFS</p> <p>DTNGAVKYFTVVVREADGSDELKPEQQHPLPSY</p> <p>LEYRHNASIRVYQTNFYASKCAENPNSNSKSFNI</p> <p>KLGAEMESLGGKCDPTQKFCDGPLKPHTAYRI</p> <p>SIRAF TQLFDEDLKEFTKPLYSDTFFSLPITTESEP</p> <p>LFGAIEGVSAGLFLIGMLVAVVALLICRQKVSHG</p> <p>RERPSARLSIRDRPLSVHLNLGQKGNRKTSCEPIK</p> <p>INQFEGHFMKLQADSNYLLSKEYEELKDVGRNQ</p> <p>SCDIALLPENRGKNRYNNILPYDATRVKLSNVDD</p> <p>DPCSDYINASYIPGNFRREYIVTQGPLPGTKDDF</p> <p>WKMVWEQNVHNIVMVTQCVEKGRVKCDHYW</p>

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				PADQDSL YYGDLILQMLSES VLP EWTIREFKICGE EQLDAHRLIRHFHYTVWPDHGV PETTQSLIQFVR TVRDYINRSPGAGPTVVHCSAGVGRGTGTFIALDR ILQQLDSKDSVDIYGAV\HDLRLHRVHMVQTEC QYVYLHQCVRDVLRARKLRSEQENPLFPYIENV NPEYHRDPVYSRH
3452	A	63	1073	FFRSSDNGSPIRQYE/HSTPAHQGPVMGLEGS/ ARNSQLRIVLVGKTGAGKSATGNSILGRKVFHSG TAAKSITKKCEKRSSSWKETELVVVDTPGIFDTE VPNAETSKEIIRCILLTSPGPHALLLVPLGRYTEE EHKATEKILKMFGERARSFMIIFTRKDDLGD TN LHDYLRAPEDIQDLMDIFGDRYCALNNKATGA EQEAQRAQLLGLIQRVVRENKEGCYTNRMYQR AEEEIQKQTQAMQELHRVELEREKARIREEYBEK IRKLEDKVEQEKRRKKQMEKKLAEQEAHYAVRQ QRARTEVESKDGILELIMTALQIASFILLRLFAED
3453	A	2674	514	GPITFLKKKAKMKDMPLRIHVLLGLAITTLVQAV DKKVD C PRLCTCEIRPWFTPRSIYMEASTVDCND LGLLTFPAPRLPANTQILLQTNNIAKIEYSTDFPV NL TGLDLSQNNLSSVTNINGKKMPQLLSVYLEEN KLTELPEKCLSELSNLQELYNHNLLSTISPGAFIG LHNLLRLHLNSNRLQMINSKWFDALPNLEILMIG ENPIRIKDMNFKPLINLRSLVIAGINL TEIPDNAL VGLENLESISFYDNRLIKVPHVALQKV VNLKFLD LNKNPINRIRRGDFSNMLHLKELGINNMP ELISID SLAVDNLPDLRKIEATNNPRLSYIHPNAFFRLPKL ESLMLNSNALSALYHGTIESLPNLKEISHSNPIRC DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGG NVRQVHFRDMMEICLPLIAPESFSPNLNVEAGSY VSFHCRA TAEPQPEIY WITPSGQKLLPNTLTDKF YVHSEGLDINGVTPKEGGLYTCIATNLVGADLK SVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSW KASSKILKSSVKWTA FVKTENSHAAQSARIPSDV KVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVT TKGLHPDQKEYEKNNTTTLMA CLGGLLGIIGVIC LISCLSP EMNCDGGHSYVRNYLQKPTFALGELY P PLINLWEAGKEKSTSLKVKATVIGLPTNMS
3454	A	1844	244	ERYLFATYVAPSATLDIGLQQEKKK EYMKIOPP FEDLFDTAEEYILL LLEPWTKMVKSDQIAYKKV ELVEETRQLDSTYFRKLQALHKETFSKKAEDTTC EIGTGILSLSNVSKRTEYWDNVPAEYKHFKFSDL LNNKLEFEHFRQFLETHSSSMDLMCWTDIEQFRR ITYRDRNQ RKA KSIYIKNKYLNKKYFFGPNSPAS LYQQNQVMHLSGGWGKILHEQLDAPVLVEIQK HVQNRL ENVWLPFLASEQFAARQKIKVQMKDI AEELL LQKA EKKIGVWKPVESK WISSCKIIAFRK ALLNPVTSRQFQRFVALKGDLL ENGLLFWQEVQ KYKDLCHSHCDESVIQKKITTIINCFINSSIPPALQI DIPVEQAQKIIHRKELGPYVFREAQM TFLGV MF KFWPQFCEFRKNLTDENIMSVLERRQEYNKQKK KLAVL/QNDEKSGKDGIKQYANTS VPAIKTALLS DSFLGLQPYGRQPTWCYSKYIEALEQERILLKIQE ELEKISCLQACNLSQILRLALQLCL
3455	A	228	3330	APTAQAMMSFGGADALLGAPFAPLHGGGSLHY ALARKGGAGGTRSAAGSSSGFHSWTRTSVSSVS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ASPSRFRGAGAA SSTDSLDTLSNGPEGCMVAVA TSRSEKEQLQALNDRFAGYIDKVRQLEAHNRSLE GEAAALRQQQAGRSAMGELYEREVREM RGA VL RLGAARGQLRLEQEHLEDIAHVQRQLDDEARQ REEAEEAARALARFAQEAEAA RVDLQKKAQAL QEECGYLRRHHQE EVGELLGQIQGSGAAQAQM QAETRDALKCDVTSALREIRAQLEGHAVQSTLQ SEEWFRVRLDRLSEA AKVNTDAMRSAQEITEY RRQLQARTTELEALKSTKDSL ERQRSELEDRHQ DIASYQEA IQQLDAELRNTKWEMAAQLREYQDL LNVKMALDIEIAAYRKLL EGEECRIGFGPIPSLP EGLPKIPSVSTHIKVKSEEKIKVVEKSEKETVIVEE QTEETQVTEEVTEEDKEAKEEEGKEEEGGEEEEE AEGGEEETKSPPAEAA SPEKEAKSPVKEEAKSP AEAKSPEKEEAKSPA EVKSPEKAKSPA KEEAKSP PEAKSPEKD GKGQNFQAEVKSPEKAKSPA KEEAK SPAEAKSPEKAKSPVKEEAKSPA EAKSPVKEEAK SPAEVKSPEKAKSPTKEEAKSPEKAKSPEKAKSP EKEEAKSPEKAKSPVKA EAKSPEKAKSPVKA EA KSPEKAKSPVKEEAKSPEKAKSPVKEEAKSPEKA KSPVKEEAKTPEKAKSPVKEEAKSPEKAKSPEKA KTL DVKSPEAKTPAKEEARSPADKFPEKAKSPVK EEVKSPEKAKSPLKEDAKAPEKEIPKKEEVKSPV KEEKPKQEVKVKEPPKKA EEEKAPATPKTEEEK DSKKEEAPKKEAPKPKVEEKK EPAVEKPKESKV EAKKEEAEDKKK VPTPEKEAPAKVEVKEDAKPK EKTEVAKKEPDDAKAKEPSKPAEKKEAAPEKKD TKEEKAKKPEEKPKTEAKAKEDDKTLSKEPSK KA EKA EKSSSTDQKDSKPPEKAT EDKAAKKGK
3456	A	258	1463	YLSFIPGHASKSAPMNGHCFAENGPSQKSSLPLPL IPPSEN LGPHEEDQVVC GFKKLT VNGVCASTPPL TPIKNPSLFP CAPLCERGSRLPPL PISEALSLDDT DCEVEFLTSSD TDFLLEDSTLSDFKYD VPGRRSF RGCGQIN YAYFDTPA VSAADLSYVSDQNGVGP DPNPPPQTHRRLLRRSHSGPAGSFNKP AIRISNCCI HRASPNSEDEKPEVPPRVPIPPRPVKPDYRRWSA EVTSSTYSDEDRPPKVPPREPLSPNSRTPSPKSLP SYLNGVMPPTQSFAPDPKYVSSKALQRQNSEGS ASKVPCILPIIENGKKVSSTHYLLPERPPYLDKY EKFFREAKKKNGGAQIQPLPADCGISSATEKPDS KTKMDLGGHVKRKHL SYVGT
3457	A	2	4869	FILSSSSASSEHFHHHSFGNWWPGSFKGHRMS LPFYQRCHQHYDLSYRNKDVRSTVSHYQREKKR SAVYTQGSTAYSSRSSAAHRRESEAFRRASASS QQASQHALSSEVSRKAASAYDYGSSHGLTDS LLLDDYSSKLSPKPKRAKHSLLSGEEKENLPSDY MVPIFSGRQKHVSGITDTEERIKEAAA YIAQRNL LASEEGITPKQSTASKQTTASKQSTASKQSTASK QSTASRQSTASRQSVVSKQATSALQQEETSEKKS RKVVIRGKAERLSLRKTLEETETYHAKLNEDHLL HAFEFIKPRSHTVWEKENVKLHCSIAGWPEPRV TWYKNQVPINVHANPGKYIIESRYGMHTLEINAC DFEDTAQYRASAMNVKGELSA YASVVVKRYKG EFDETR FHAGASTMPLSFGVTPYGYASRFEIHF DKFDVSFGREGETMSLGCRVVITPEIKHFQPEIQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				<p>WYRNGVPLSPSKWVQTLWSGERATLTFSHLNKE DEGLYTIRVRMGEYYEQYSAYVFVRDADAEIEG APAAPLDVKCLEANKDYIIISWKQPAVDGGSPIL GYFIDKCEVGTDSWSQCNDTPVKFARFPVTGLIE GRSYIFRVRAVNKMIGFSPRVSEPVAALDPAEK ARLKS/PPLSTLDWT/VIVTEEEPSEGIVPGPPTDLS VTEATRSYVVLWSWKPPGQRGHEGIMYFVEKCEA GTENWQRVNTELPVKSPRFALFDLAEGKSYCFR VRCSNSAGVGEPSEATEVTVVGDKLDIPKAPGKI IPSRNTDTSVVVSWEESKDAKELVGYIEANVA GSGKWEPCNNNPVKTHRFTCHGLVTGQSYIFRV RAVNAAGLSEYSQDSEAIEVKAIAAPPSPCDITC LESFRDSMVLGWKQPKIGGAIEITGYVNYREV IDGVPGKWREANVKA VSEEAYKISNLKENMIV QFQVAAMNMAGLGAPSAVSECFKCEEWTIAVP GPPHSLKCSEVRKDSLVLQWKPPVHSGRTPVTG YFVDLKEAKAKEDQWRGLNEAAIKNVYLKVRG LKEGVSYYFRVRAINQAGVGKPSDLAGPVVAET RPGTKEVVVNVDGDISLNFECDKMTPKSEFS WSKD YVSTEDSPRLEVESKGNKTKMTFKDLGM DDLGIYSCDVTDTDGIASSYLIDEEELKRLALSH EHKFPTVPVKSELA VEILEKGQVRFWMQAEKLS GNAKVNYIFNEKGIFEGPKYKMHIDRNTGIIEMF MEKLQDEDEGTYTFQLQDGKATNHSTVVLVGD VFKKLQKEAEFQRQEWIRKQGPHFVEYLSWEVT GECNVLLKCKVANIKKETHIVWYKDEREISVDE KHDFKDGICTLLITEFSKKDAGIYEVILKDDRGRK DKSRLKLVDFAFKELMMEVCKKIALSATDLKIQ STAEGIQLYSFVTYYVEDLKVNWSHNGSAIRYSD RVKTGVTGEQIWLQINEPTPNDKGKYVMELFDG KTGHQKTVDLSGQAYDEAYAEFQRLKQAAIAEK NRARVLGGLPDVVTIQEGKALNLT CNVWGDPPP EVSWLKNEKALASDDHCNLKFEAGR TAYFTING VSTADSGKYGLVVKNKYGSETSDFTVSVFIPPEE ARMAALES LKGGKKAK</p>
3458	A	3963	827	<p>LSRSSDNNNTLGRNVMSTATSPLMGAQSFPNL TTPGTTSTVTMSTSSVTSSSNVATATTVLSVGQS LSNTLTSTSTSSSED TGQAEYSLYDFLDSCRA STLLAELDDDEDLPEPDEEDDENEDNQEDQEY EEVMILRRPSLQRRAGSRSDVTHHAVTSQLPQVP AGAGSRPIGEQEEEEYETKGGRRRTWDDDYVLK RQFSALVPAFDP RPGR TNVQQTDDLEIPPGTPHS ELLEVECTPSRLALTLKVTGLGTTREVELPLTN FRSTIFYVQKLLQLSCNGNVKSDKLRIWEPTY TIMYREMKDSKKEKENGKMGCSIEHVEQYLG TDELPKNDLITYLQKNADAFLRH WKLTGTNKS IRKNRNC SQLIAAYWDLG\EHGTK\SGLNQGAIST LQSSDILNLTK EQQAKAGNGQNSCGVEDVLQL LRILYIVASDPYSRISQEDGDEQPQFTFPPEFTS/ KKITTKILQQIEPLALASGALPDWCEQLTSKCPF LIPFETRQLYFTCTAFGASRAIVWLQNRREATIVE RTRTTSSVRRDDPGEFRVGR LKHERVKVPRGESL MEWAENVMIHADRKSVLEVEFLGEEGTGLGPT LEFYALVAAEFQRTDLGAWLCDDNFPDDES RHV DLGGGLKPPGYVQRSCGLFTAPFPQDSDELERI</p>

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TKLFHFLGIFLAKCIQDNRLVDLPISKPFCKLMCM GDIKSNMSKLIYESRGDRDLHCTESQSEASTEEG HDSL SVGSFEEDSKSEFILDPPKPKPPAWFNGILT WEDFELVNPHRARFLKEIKDLAIKRRQILSNKGL SEDEKNTKLQELVLKNPSGSGPPLSIEDLGLNFQF CPSSRIYGFTA VDLKPSGEDEMITMDNAEEYVDL MFDFCMHTGIQKQMEAFRDGFNKVFPMEKLSFF SHEEVQMILCGNQSPSWAAEDIINYTEPKLGYTR DSPGFLRFVRVLCGMSSDERKAFLQFTTGCSLTP PGGLANLHPRLTVVRKVDATDASYPSVNTCVHY LKLPEYSSEEIMRERLLAATMEKGFHLN
3459	A	88	603	SCGPRGLASLGLGFSGRCDDQNKGRS\DGPEAQA EACSGERTYQELLVNQNPILAQLASRRLTRKLYK CIKKAVKQKQIRRGVKEVQKFVNKGEKGIMVLA GDTLPIEVYCHLPVMCEDRNLPYVYIPSKTDLGA AAGSKRPTCVIMVKPHEEYQEA YDECLLEE VQSL PLPL
3460	A	139	1997	QVTNMSDKSELKAELERKKQRLAQIREKKRKE EERKKKETDQKKEAVAPVQEEEDLEKKRREA LLQSMGLTPESIVPPPMSPSSKSVSTPSEAGSQD SGDGAVGSRRGPIKLGMAKITQVDFPPREIVTYT KETQTPVMAQPKEDDEEDDDVAPKPPIEPEEEK TLKKDEEN\DSKAPPHELTEEEKQQLHSEEFLSFF DHSTRIVERALSEQINIFFDYSGRDF/ENDKEGEIQ AGAKLSLNRQFF\DER\WSKASGWVSCLDWSSQ YPELLVASYN\NEDAPHEPDGVALVWNMKYK KTTPEYVFHCQSAVMSATFAKFHPNLVVG GTYS GQIVLWDNRSNKRTPVQRTPLSAAAH\THPVYCV NVVGTQNAHNLISISTDGKICSWSLDMLSH PQDS MELVHKQSKAVAVTSMSPVGDVNNFVVGSEE GSVYTACRHGSKAGISEMFEGHQGPITGIHCHAA VGAVDFSHLYVTSSFDWTVKLWTTKNNKPLYSF EDNAGYVYDVMWSP\THPALFACVDGMGRDL WNLNNDTEVPTASISVEGNPALNRVRWTHSGRE IAVGDEGQIVYDVGEQIAVPRNDEWARFGR TL AEINANRADAEEEAATRIPA
3461	A	139	1997	QVTNMSDKSELKAELERKKQRLAQIREKKRKE EERKKKETDQKKEAVAPVQEEEDLEKKRREA LLQSMGLTPESIVPPPMSPSSKSVSTPSEAGSQD SGDGAVGSRRGPIKLGMAKITQVDFPPREIVTYT KETQTPVMAQPKEDDEEDDDVAPKPPIEPEEEK TLKKDEEN\DSKAPPHELTEEEKQQLHSEEFLSFF DHSTRIVERALSEQINIFFDYSGRDF/ENDKEGEIQ AGAKLSLNRQFF\DER\WSKASGWVSCLDWSSQ YPELLVASYN\NEDAPHEPDGVALVWNMKYK KTTPEYVFHCQSAVMSATFAKFHPNLVVG GTYS GQIVLWDNRSNKRTPVQRTPLSAAAH\THPVYCV NVVGTQNAHNLISISTDGKICSWSLDMLSH PQDS MELVHKQSKAVAVTSMSPVGDVNNFVVGSEE GSVYTACRHGSKAGISEMFEGHQGPITGIHCHAA VGAVDFSHLYVTSSFDWTVKLWTTKNNKPLYSF EDNAGYVYDVMWSP\THPALFACVDGMGRDL WNLNNDTEVPTASISVEGNPALNRVRWTHSGRE IAVGDEGQIVYDVGEQIAVPRNDEWARFGR TL AEINANRADAEEEAATRIPA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3462	A	2	2643	TAPEFSRSTHASAHASVARVLRNREIAQLKKEQR RQEFQIRALESQKRQEMVLRRKTQEVSA LRRL AKPMSE RVAGRAGLKPPMLDSGA EVSASTTSSE AESGARSVSSIVRQWNRKINHFLGDHPAPT VNGT RPARKKFQKKGASQSFSKAARLKWQSLERRIID VMQRM TIVNLEADMERLIK KREELFLLQEALRR KRERLQAESP EEEKGLQELAE EIEVLAANIDYND GITDCQATIVQLEETKEELDSTDTSVISSCSLAE ARLLDNFLKASIDKGLQVAQKEAQIRLLEGRLR QTD MAGSSQNHL LLDALREKAE AHPELQALIYN VQQENGYASTDEEISEFSEGSFSQSFTMKGSTSH DDFKFKSEPKLSAQMKAVSAECLGPPLDISTKNI TKSLASLVEIKEDGVGFSVRDPYYRDRVSRTVSL PTRGSTFPRQSRATETSP LTRKSYDRGQPIRSTD VGFTPPSSPPTRP RNDNRNVFSRLTSNQSQGSALD KSDDSDSSLSEVL RGIISPVGGA KGARTAPLQCV SMAEGHTKPI LC LDATDELLFTGSKDRSCKMWN LVTGQEIAALKGHPNNVVS IKYCSHGLVFSVST SYK VWDIRDSAKCIRTLTSSGQVISGDACAATST RAITSAQGEHQINQIALSPSGTMLY AASGNAVRI WELSRFPVGKLTGHIGPVMCLTVTQTASQHD L VVTGSKDHYVKMFELGECVTGTIGPTHNFEPH YDGIECLA IQGDILFSGSRDNGIKK WDL DQQELIQ QIPNAHKDWVCALAFIPGRPMLLSACRAGVIKV WNVDFNFTPIGEIKGHDSPINAICTNAKHIFTASSG CRVKVWVNYVPGLTPCLPRRVLAIKGRATTLP
3463	A	198	3146	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFA GVYRAESIHTGLEVAIKMIDKKAMYKAGMVQR VQNEVKIHCQLKHPSILELYNYFEDSNYVYLVE MCHNGEMNRYLKNRVKPFSENEARHF MHQIITG MLYLHSHGILHRDLTSLNLLTRNMNIK IADFGL ATQLKMPHEKH YTL CGTPNYISPEIATRS AHGLE SDVWSLGCMFY TLLIGRPPFD TDTVKNTLNKV LADYEMPTFLSIEAKDLI HQLLRRNPADRLSLSSV LDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAI TASSSTSISGSLFDKRRL LIGQPLPNKMTVFPKNK SSTDFSSSGDGNSFYTQWGNQETSNSGRGRVIQD AEERPHSRYLRRAYSSDRSGTSNSQSQA KTYTM ERCHSAEMLSVSKRSGGGENEERYSP TDNNANIF NFFKEKTSSSSGSFERPDNNQALS NHLCPGKTPFP FADPTPQTETVQQWFGNLQINAH LRKTTEYDSIS PNRDFQGH PDLQKDTSKNAWTDTKVKKNSDAS DNAHSVKQQNTMKYMTALHSKPEIIQQECVFGS DPLSEQSKTRGMEPPWGYQNR TLRSTSP LVAHR LKPIRQKTKKAVVSILDSEEVVELVKEYASQEY VKEVLQISSDGN TITTYYPNGGVRGFPLADRPPSP TDNISRYSFADNLPEKYWRKYQYASRFVQLVRS KSPKIT YFTRYAKCILMENS PGADFEVWFYDGV KIHKTEDFIQVIEKTGKSYTLKSESEVNSLK EEEK MYMDHANEGHRI CLALESIISEEERKTRSAFFPII IGRKPGSTSPKALSPPSVDSNYPTRDRASFNRM VMHSAASPTQAPILNPSMVTNEGLGLTTTASGTD ISSNSLKDCLPKSAQLLKS VFVKNVGWATQ L TS GAVVWVQFNDGSQLVVQAGVSSISY TSPNGQITTR YGENEKL PDYIKQKLQCLSSILLMFNPTPNFH

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3464	A	14	348	AVRTVSGTSLGPRSHSRSPGRCHCFSAVTFSSPRL AASEAPDPMEEWDVPQMKKEVESLKYQLAFQR EMASKTIPELLKWIEDGIPKDPFLNPDLMKNNPW VIEKGKCTIL
3465	A	5537	405	VRKLDREVRGAWWRGAWARHPRQEAGEHAHR RKGHAETPRGRKGRAGRSAAVVELPARRSL ETSRAAAAMAKDSPSPPLGASPKKPGCSSPAAAV LENQRRELEKLRAELEAERAGWRAERRRFAARE RQLREEAERERRQLADRLRSKWAEQRSRELRLQ QEEMQREREAEIRQLLRWKEAEQRQLQQLHRE RDGVVRQARELQRQLAEELVNRGHCSRPGASEV SAAQCRCRLQEVLAQLRWQTDGEQAARIRYLQ AALEVERQLFLKYLAHFRGHPALSGSPDPQAVH SLEEPLOTSSGSCHAPKPACQLGSLDSLAEVG VRSRLGLVSSACSSSPDGLLSTHASSLDCFAPAC SRSLDSTRSLPKASKSEERPSSPDTSTPGSRRLSPP PSPLPPPPPSAHRKLSNPRGGEGSESQPCVLTPTS PPGLGHHeliklnwllakalwvlarrcytlqee NKQLRRAGCPYQADEKVKRLKVKRAELTGLAR RLADRARELQETNLRAVSAPIPGESCAGLELCQV FARQRARDLSEQASAPLAKDKQIEELRQECHLLQ ARVASGPCSDLHTGRGGPCTQWLNVRDLDRQL RESQREVLRQLRQLMLQQGNNGGAWEAGGQSA TCEEVRRQMLALERELDQRRRECQELGAQAAPA RRRGEEAETQLQAALLKNAWLABENGRLQAKT DWVRKVEAENSEVRGHLGRACQERDASGLIAEQ LLQQAARGQDRQQQLQRDPQKALCDLHPSWKEI QALQCRPGHPPEQPWETSQMPESQVKGSRPKF HARAEDYAVSQPNRDIQEKREASLEESPVALGES ASVPQVSETVPASQPLSKKTSSQSNSSSEGSMWA TVPSSPTLDRDTASEVDDLEPDSVSLALEMGSA APAAPKLKIFMAQYNNPFEGPNDHPEGELPLTA GDYTYIFGDMDEDGFYEGELEDGRRGLVPSNFVE QIPDSYIPGCLPAKSPDLGPSQLPAGQDEALEEDS LLSGKAQGVVDRGLCQMVRVGSKEVATEILDT KTEACQLGLLQSMGKQGLSRPLLGTKGVLRMAP MQLHLQNVATSANITWVYSSHRHPHVYVYLD REHALTPAGVSCYTFQGLCPGTHYRARVEVRLP RDLLQVYWGTMSSVTFDTLLAGPPYPPLDVLV ERHASPGVLVSWLPVTIDSAGSSNGVQVTGYA VYADGLKVCEVADATAGSTLLEFSQLQVPLTWQ KVSVRTMSLCGESLDSVPAQIPEDFFMCHRWPET PPFSYTCGDPSTYRVTFPVCQKLSLAPPSAKASP HNPGSCGEPQAKFLEAFFEPPRRQSPVSNLGSE GECPSGAGSQAQELAEAWEGCRKDLLFQKSPQ NHRPPSVSDQTGEKENCYQHMGTSKSPAPGFHIL RTECGPRKEPCQEKAALERVLRQKQDAQGFTTP QLGASQQYASDFHNVLKEEQEALCLDLWGTER EERREPEPHSRQGQALGVKRGCLHEPSSALCPA PSAKVIKMPRGGPQQLGTGANTPARVFVALSDY NPLVMSANLKAEEELVFQKRQLLRVWGSQDT HDFYLSNCRQVGNIPGRLVAEMEVEGTQDTRR WRSPAQGHLPVAHLEDFQGLTIPQGSSSLVLQGN SKRLPLWTPKIMIAALDYDPGDGQMGQGKGRIL ALRAGDVVMVYGPMDDQGFYYGELGGHGRGL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VPANLRIKMSSQGH
3466	A	1	1111	MSKPPDLLRLLRGAPRQRVCTLFIIIGFKFTFFVSI MIYWHVVGEPKEKGQLYNLPAEIPCPTLTPPTPP SHGPTPGNIFFLETSDRTNPNFLMCSVESAARTH PESHVLVLMKGLPGGNASLPRHLGISLLSCFPNV QMLPLDLRELFRDTPADWYAAVQGRWEPLYLL PVLSDASRIALMWKFGGIYLDTFIVLKNLRNLT NVLGTQSRVYVNLGAFLAFERRHEFMALCMRDFV DHYNGWIWGHQGPQLLTRVFKKWCSIRSLSAESR ACRGVTTLPPFAFYPIPWQDWKKYFEDINPEELP RLLSATYA VHVWNKKŠQGTRFEATSRALLAQLH ARYCPTTHE/DHENVLVKGPAGHLPNLLLMGHW
3467	A	1	2175	MAKVILKQSKQCKNLLTCKVAQVCPVCGCLHC YFWWLSGLESRPSSPLIDIKPIEFGVLSAKKEPIQ PSVLRRTYNPDYFRKFEPHLYSLDSNSDDVDLSL TDEEILSKYQLGMLHFSTQYDLLHNHLLTVRVIEA RDLPPISHDGSRQDMAHSNPYVKICLLPDQKNS KQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLLL TVVDFDKFSRHCVIGKVSVPCEVDLVKGGHW WKAHDSQFSAPGLPADQQFFADLFSGLVLPNQL LGRVWFASQPASLPVGSCLIDFPRLDIVLRGEYG NLLEAKQQLRVEGEMLFIPARAANLPVNNKPVM LLSLVFAPTWLGLSFYDSRTTSLHLPARQIQLPSL QRGEGEAMLSALTLFSRSPLEQNIQPLVLSLLHL CGSVVNMPPGNSQPRGDFLYHSICTWVQDNYAQ PLTRESVAQFFNITPNHLSKLFAQHGTMRFIEYVR WVRMAKARMILQKYHLSIHEVAQRCPGPDSDYF CRVFRQFGMDYVDILQIHRWDYNTPIETLEAL NDVVKAGKARYIGASSMHASQFAQALELQKQH GWAQFVSMQDHYNLIYREEEREMLPLCYQEGV AVIPWSPLARGRLTRPWGETTARLVSEVGVKNL YKESDENDAQIAERLTGVSEELGATRAQVALAW LLSKPGIAAPIIGTSREEQLDELLNAVDITLKPEQI AELETYPYKPHPVVGFK
3468	A	147	3209	ALPLPLPTLYPGMSRRKQRKPQQLISDCEGPSASE NGDASEEDHPQVCAKCCAQFTDPTFLAHQNAAC STDPPVMVIIGGQENPNSSASSEPRPEGHNNPQ VMDTEHSNPPDSGSSVPTDPTWGPERRGEESSGH FLVAATGTAAGGGGGLILASPKLGATPLPPESTP APPPPPPPPPPGVSGHLNIPLILEELRVLQQRQI HQMOMTEQICRQVLLGSLGQTVGAPASPSLPL GTGTASSTKPLPLFSPIKPVQTSKTLASSSSSSSS SSGAETPKQAFFHLYHPLGSQHPFSAGGVGRSHK PTPAPSPALPGSTDQLIASPHLAFSTTGLLAAQC LGAARGLEATASPGLLKPKNGSGELSYGEVMGP LEKPGGRHKCRFCAKVFGSDSALQIHLRSHTGER PYKCNVCGNRFTTRGNLKVHFHRHREKYPHVQ MNPHVPHELDYVITSSGLPYGMSVPPEKAEAAA ATPGGGVERKPLVASTTALSATESLTLLSTAGT ATAPGLPAFNKFVLMKAVEPKNKADENTPPGSE GSAISGVAESSTARMQLSKLVTSLPSWALLTNH FKSTGSFPLPLCARALGASPSSETSKLQQLVEKID RQGAVAVTSAASGAPTTAPAPSSSASSGPNQCV ICLRVLSCPRALRLHYGQHGGGERPFKCKVCGRAF STRGNLRAHFVGHKASPAARAQNSCPICQKKFT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NAVTLQQHVRLMHLGGQIPNGGTALPEGGGAAQ ENGSEQSTVSGAGSFPPQQSQQPSPEEELSEEEEE EDEEEEDVTDEDSLAGRGSESGGEKAISVRGDS EEASGAEEEVGTVAATAAGKEMDSNEKTTQQS SLPPPPPSLDQPPMEQGSSGVLGGKEEGGKP ERSSSPASALTPEGEATSVTLVEELSLQEAMRKEP GESSSRKACEVCGQAFPSQAALVEEHQKTHPKEG PLFTCVFCRQGFLERATLKKHMLLAHHQVQPPFA PHGPQNIAALSLVPGCSPSITSTGLSPFPRKDDPTI P
3469	A	3	5664	NLRPLSFALFLGDPNMANLEESFPRGGTRKIHKP EKAFAQSVEQDNLFDISTEEGSTKRKKSQKGP TKKLKIEKRESSKSAREKFEILSVESLCEGMRLG CVKEVNELELVISLPNGLQGFVQVTEICDAYTKK LNEQVTQEQLKDLLHLPELFSFGMLVRCVSSSL GITDRGKKS VKLSLNPKNVNRVLSAEALKPGML LTGTVSSLEDHGYLVDIGVDGTRAFLLKAEY IRQKNKGAKLVGQYLN CIVEKVKNGGGVVSLS VGHSEVSTAIATEQQSWNLNNLLPGLVVKAQVQ KVTPFGLTLNFLTFFTGVVDFMHLDPKKAGTYFS NQAVRACILCVHPRTRVHLSLRPIFLQGRPLTR LSCQNLGAVLDDVPVQGFFKKAGATFRLKDGVL AYARLSHLSDSKNVFNPEAFKPGNTHKCRIDYS QMDLALLSLRTSHIAQYLRHYHDIEGAVVKG VLTIKSYGMLVKVGEQMRGLVPPMHLADILMK NPEKKYHIGDEVKCRVLLCDPEAKKLMMLTKKT LIESKLPVITCYADAKPGLQTHGFIURVKDYGCIV KFYNNVQGLVPKHELSTEYIPDPERVFYTGQVV KVVLNCEPSKERMILLSFKLSSDPEPKKEPAGHS QKKGKAINIGQLVDVKVLEKTKDGLEVAVLPHN IRAFPTSHLSHDVANGPLLHHWLQAGDILHRVL CLSQSEGRVLLCRKPALVSTVEGGQDPKNFSEIH PGMLLIGFVKSIKDYGVFIQLPSGLSGLAPKAIMS DKFVTSTSDHFVEGQTVAAKVTNVDEEKQRMML SLRLSDCGLGLAITSLLLLNQCLEELQGVRSML SNRDSVLIQTLAEMTPGMFLDLVVQEVLEDGSV VFSGGPVVDLVLKASRYHRAGQEVESGQKKKV ILNVDLLKLEVHVS LHQDLVNRKARKLRKGSE HQAIVQHLEKSFAIASLVETGHAAFSLTSHLND TFRDSEKLQVGQGVSLTLKTTEPGVTGLLLAVE GPAAKRTMRPTQKDSETVDEDEEVDPALTVGTI KKHTLSIGDMVTGTVKSIPHTHVVTLEDGIIGCI HASHLDDVPEGTSPTTKLVGKTVTARVIGGRD MKTFKYLPISHPRFVRTIPELSVRPSELEDGHTAL NTHSVSPMEKIKQYQAGQVTCFLKKYNVVK WLEVEIAPDIRGRIPLLLTSFKVLKHPDKKFRV GQALRATVVGPDSSKTFLCLSLTGPHKLEEGEVA MGRVVKVTPNEGLTVSFFFGKIGTVSIFHMSDSY SETPLEDFVPQKVRCYILSTADNVLTSLRSSRT NPETKSKVEDPEINSIQDIKEGQLLRGYVGSIQPH GVFFRLGPSVVG LARYSHVSQHSPSKKALYNKH LPEGKLLTARVLRNLHQKNLVELSFLPGDTGKPD VLSASLEGQLTKQEERKTEAEERDQKGEKKNQK RNEKKNQKGQEEVEMPSKEKQPPQKPAQKRG GRECRESGSEQERVSKPKKAGLSEEDDSLVDV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				YYREGKEEAEETNVLPKEKQTKPAEAPRLQLSSG FAWNVGLDSLTPALPLAESSDSEDEKPHQATI KKSCKERELEKQKA EKELSRTEEALMDPGRQPE SADDFDRLVLSSPNSSILWLQYMAFHLQATEIEK ARAVAERALKTISFREEQEKLNVWVALLNLENM YGSQESLTKVFERAVQYNEPLKVFLHLADIYAKS EKFQAEAGELYNRMLKRFRQEKAVWIKYGAFLLR RSQAAASHRVLQRALECLPSKEHVDVIKFAQL EFQLGDAERAKAIFENTLSTYPKRTDVWSVYID MTIKHGSQKDVRDIFERVIHLSLAPKRMKFFFKR YLDYEKQHGTEKDVQAVKAKALEYVEAKSSVL ED
3470	A	2334	1226	TAAAPVAPGTMDDATVLRKKGYIVGINLGKGSY AKVKSAYSERLKFNVAVKIARKKTPDTDFVERFL PREMDILATVNHGSIKTYEIFETSDGRIYIMELG VQGDLLFIKCGALHEDVARKMFRQLSSAVKY CHDLDIVHRDLKCNLLLDKDFNIKLSDFGFSKR CLRDSNGRIILSKTFCGSAA YAAPEVLQSIYPQK VYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQK EHRVDFPRSKNLTCECKDLIYRMLQPDVSKRLH IDEILSHSWLQPPKPKATSSASFKEGEGKYRAE CKLDTKTGLRPDHRPDHKLGAKTQHRLLVVPEN ENRMEDRLAETRAKDHHSAGAEVGKAST
3471	A	537	148	TERGAPQHPTLPLPSLTPSSVHTGQPKTTPSVILFL PSCEEPQANKATLVCLMNN/YYPGILMVTWKAD GTLITQSVEKTPPSKQSNKYVASSYLSLTPEQW RSRRSYSCQVMQEGSTVEKSVAPAECS
3472	A	1	2272	DKPTRHKTYLSSSWAKMAAAEGPVG DGELWQT WLPNHVVFLRLREGLKNQSPTEAEKPASSSLPSS PPPQLLTRNVVFLGGLFLWDGEDSSFLVVRRLR GPSGGGEEPALSQYQRLLCINPPLFEIYQVLLSPT QHHVALIGIKGLMVLELPKRWGKNSEFEGGKST VNCSTTPVAERFFTSSTSLTLKHAA WYPSEILDPH VLLTSDNVIRIYSLREPQTPTNVILSEAEESLV LNKGRAYTASLGETAVAFDFGPLAA VPKTLFGQ NGKDEVVAYPLYLYENGETFLTYSLLHSPGN/I WKA VGSIAHASAAEDNYGYDACA VCLCLPCVPN ILVIATESGMLYHCVVLEGEEDDHTSEKSWDSR IDLIPSLYVFECVELELALKLASGEDDPFDSDFSC PVKLHRDPKCPSRYHCTHEAGVHSVGLTWIHKL HKFLGSDDEEDKDSLQELSTEQKCFVEHILCTKPLP CRQPAPIRGFWIVPDILGPTMICITSTYECLIWPLL STVHPASPPLLCTREDVEVAESPLRVLAEPTDSFE KHRSILQRSVANPAFLKASEKDIAPPPPECLQLLS RATQVFREQYILKQDLAKEEIQRRVKLLCDQKK KQLEDLSYCREERKSLREMAERLADKYEEAKEK QEDIMNRMKKLLHSFHSLEPVLSDSERDMKKEL QLIPDQLRHLGNAIKQVTMKKDYQQQKMEKVL SLPKPTIILSAYQRKCIQSILKEEGEHIREMVKQIN DIRNHVNF
3473	A	1	2272	DKPTRHKTYLSSSWAKMAAAEGPVG DGELWQT WLPNHVVFLRLREGLKNQSPTEAEKPASSSLPSS PPPQLLTRNVVFLGGLFLWDGEDSSFLVVRRLR GPSGGGEEPALSQYQRLLCINPPLFEIYQVLLSPT QHHVALIGIKGLMVLELPKRWGKNSEFEGGKST

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isolucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VNCSTTPVAERFFTSSTSLTLKHAAWYPSEILDPH VVLLTSDNVIRIYSLREPQTPTNVILSEAEESLV LNKGRAYTASLGETAVAFDFGPLAAVPKTLFGQ NGKDEVVA YPL YIL YENGETFLTYISLLHSPGN/I WKAVGSIAHASAAEDNYGYDACAVLCLPCVPN ILVIATESGMLYHCVVLEGEEDDHTSEKSWDSR IDLIPSLYVFECVELELALKLASGEDDPFDSDFSC PVKLHRDPKCPSRYHCTHEAGVHSVGLTWIHKL HKFLGSDEEDKDSLQELSTEQKCFVEHILCTKPLP CRQPAPIRGFWIVPDILGPTMICITSTYECLIWPLL STVHPASPPLLCREDVEVAESPLRVLAETPDSFE KHRSILQRSVANPAFLKASEKDIA PPPEECLQLLS RATQVFREQYILKQDLAKEEIQRRVKLLCDQKK KQLEDLSYCREERKSLREMAERLADKYEEAKEK QEDIMNRMKKLLHSFHSSELVLSDSERDMKKEL QLIPDQLRHLGNAIKQVTMKKDYQQQKMEKVL SLPKPTILSAYQRKCIQSILKEEGEHIREMVKQIN DIRNHVNF
3474	A	4344	2550	DRRREPERHVRVKQRTSVLNMRLRLDKIRFRGH KRDDFLDLAESPNASDTECSDEIPLKVPRTSPRDS EELRDPAGPGTLIMATGVQDFNRTEFDRLEIKG HLEIALLEKHFLQEELRKLREETNAEMLRQELDR ERQRRMELEQKVQEV LKARTEEQMAQQPPKGQ AQASNGAERRSQGLSSRLQKWFYERFGEYVEDF RFQPEENTVETEEPLSARRLTENMRLKRGAKPV TNFVKNLSALSDWYSVYTSIAFTVYMNAVWH GWAIPFLFLAILRLSLNYLIARGWRIQWSIVPEV SEPVEPPKEDLTVSEKFQLVLDVAQKAQNLFGK MADILEKIKNLFMWVQPEITQKLYVALWAAFLA SCFFPYRLVGLAVGLYAGIKFFLIDFIFKRCPRLR AKYDTPYIWRSLPTDPQLKERSSAAVSRLQTTS SRSYVPSAPAGLGKEEDAGRFHSTKKGNFHEIFN LTENERPLAVCENGWRCCLINRDRKMPTDYIRN GVLYVTENYLCFESSKSGSSKRNVIKLVDITDI QKYKVLVLPGSGMGIAVSTPSTQKPLVFGAMV HRDEAFETILSQYIKITSAAAASGGDS
3475	A	2	1126	TAARRRQKGAAAAAETHGQAKAKSGWLKPYFF IELMESRKDITNQEELWKMKPRRNLEEDDYHLK DTGETSMLKRPVLLHLHQTAAHDEFDCPSELQH TQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLA TSHQQYFYKIPILVINKVLPMSITLLALVYLPV IAAIVQLHNGTKYKKFPHWLDKWMLTRKQFGL LSFFFAVLHAIYSLSPMRRSYRYKLLNWAYYQQ VQQNKEDALIEHDVWRMEIYVSLGIVGLAILAL LAVTSIPSVSDSLTWREFHYIQSKLGIVSLLGTIH ALIFAWNKWIDIKQFVWYTPPTFMIAVFLPIVLI FKSILFLPCLRKKILKIRHWEDVTINKTEICSQL
3476	A	143	3191	AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRL DLILCNKTA YQEVFKPENISLRNKLRELCVKLMF LHPVDYGRKAEELLWRKVYYEVIQLIKTNKKHI HSRSTLECA YRTHLVAGIGFYQHLLLYIQSHYQL ELQCCIDWTHVTDPLIGCKKPVASGKEMDWAQ MACHRCLVYLGDLSTRYQNELAGVDTELLAERFY YQALSVA PQIGMPFNQLGTLGASKYYNVEAMY CYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KKCETRKLSPGKKRCKDIKRLLVNFMYLQSLIQ PKSSSVDELSTSLCQSVLEDFNLCLFYLPSSPNLS LASEDEEEYESGYAFLPDLLIFQMVIICLMCVHSL ERAGSKQYSAIAFTLALFSLVNHVNIRLQAE EEEENPVPAFQSDGTDEPESKEPVEKEEEEDPEPP PVTPQVGEGRKSRKFSRLSCLRRRRHPPKVGDSS DLSEGFESDSSHDSARASEGSDSGSDKSLEGGGT AFDAETDSEMNSQESRSDLEMEEEEGTRSPITL PPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQM FQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCV NGDVKDPSEPAEEGSESESGESSGRSCRNERSIQ EKLQVLMAEGLLPAVKVFLDWLRTNPDLIVCA QSSQSLWNRLSVLLNLLPAAGELQESGLALCPEV QDLLEGCELPDLPSLLLPEDMALRNLPPLRAAH RRFNFDTRPPLLSTLEESVVRICCRSFGHFIARLQ GSILQFNPEVGIFVSIAQSEQESLLQQAQAQFRMA QEEARRNRLMRDMAQLRLQLEVSQLEGLSQPK AQSAMSPYLVPDTQALCHHLPVIRQLATSGRFVI IPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGN RYIRCQKEVGKSFERHKLKRQDADAWTLYKILD SCKQLTLAQGAGEEDPSGMVTITGLPLDNPVS SGPMQAALQAAAHASVDIKNVLDIFYKQWKEIG
3477	A	1	3902	MTEPRERRGYSVPPRPEVGTQATEWRVEESNFN KIFLKKDAELGRSNHLPTWDKPEDASWLPQSCL GGDAVATTGEIHEEKAWKTRALEVGQPAQRDIR RGELWGKEHGADQAIQETLEDLSSLERTLVVSES SPLGGDCQEVTTTLTVKYQVSEEVPSGTVIGKLSQ ELGREERRRQAGAAQVQLQLPQALPIQVDSEGL LSTGRRLDREQLCRQWDPCLVSFDVLATGDLALI HVEIQVLDINDHQPRFPKGEQEISESASLRTRIP LDRALDPDTGPNTLHTYTLSPSEHFALDVIVGPD ETKHAELIVVKELDREIHSFFDLVLTAYDNGNPP KSGTSLVKVNVLDSDNDNSPAFAESSLALEIQEDA APGTLLIKLTATDPDQGPNGEVEFFLSKHMPEV LDTFSIDAKTGQVILRRPLDYENPAYEVDVQAR DLGPNPIAHCKVLIKVLVDNDNIPSIHVTWASQP SLVSEALPKDSFIALVMADDLDSGNNGLVHCWL SQELGHFRLKRTNGNTYMLLTNATLDREQWPK YTLTLLAQDQGLQPLSAKKQLSIQISDINDNAPVF EKSRYEVSTRENNLPSLHLITIKAHDADLGINGK VSYRIQDSPVAHLVAIDSNTGEVTAQRSLNVEEM AGFEFQVIAEDSGQPM LASSVSVVWSLLDANDN APEVVQPVLSDGKASLSVLVNASTGHLLVPIETP NGLGPA GTDTPPLATHSSRPFLTTIVARDADSG ANGEPLYSIRSGNEAHLFILNPHTGQLFVNVTNA SSLIGSEWELEIVVEDQGSPLQTRALLRVMFVTS VDHLRDSARKPGALSMSMLTVICLAVLLGIFGLI LALFMSICRTEKKNRAYNCREAESTYRQPKR PQKHIQKADIHLVPVLRGQAGEPCEVGQSHKDV DKEAMMEAGWDPCLQAPFHLTPTLYRTLNRQG NQGAPAESREVLQDTVNLLFNHPRQRNASREN NLPEPQPATGQPRSRPLKVAGSPTGRLAGDQGS EAPQRPPASSATLRRQRHLNGKVSPEKESGPRQI LRSVLRLSVAFAERNPVEELTVDSPPVQQISQLL SLLHQGFQPKPNHRGNKYLAKEGSGRSAPDITD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEE LSSLLDPSTGLALDRLSAPDPAWMARLSLPLTTN YRDNVISPDAAA TEEPRTFQTFGKAEAPELSPTG TRLASTFVSEMSLLEMLLEQRSSMPVEAASEAL RRLSVCGRTLSDLATSAASGMKVQGDPGGKTG TEGKSRGSSSSSRCL
3478	A	13	1620	TLPPPGNSGCHRLCFPEFEFLQVTKMEFSGRKWR KLRLAGDQRNASYPHCLQFYLPQPSSENISLIEFEN LAIDRVKLLKSVENLGVS YVKGTEQYQSKLESEL RKLKFSYRENLEDEYEPRRRDHISHFILRLAYCQS EELRRWFIQQEMDLLRFRFSILPKDKIQDFLKDSQ LQFEAISDEEKTREQEIVASSPSLSGLKLGFSIY KIPFADALDLFRGRKVYLEDGFA YVPLKDIVAIL NEFRAKLSKALALTARSLPAVQSDERLQPLNLHL SHSYTGQDYSTQGNVGKISLDQIDLLSTKSFPPC MRQLHKALRENHHLRHGGRMQYGLFLKGIGLT LEQALQFWKQEFIKGKMDPKFDKGYSYNIRHS FGKEGKR TDYTPFSCLKILSNPPSQGDYHGC PFR HSDPELLKQKLQSYKISPGGISQILDVKGTHYQ VACQKYFEMIHTVDDCGFSLSHPNQYFCESQRI LNGGKDIKKEPIQETPQPKPSVQTKDASSALA SLNSSLEMDMEGLEDYFSEDS
3479	A	698	138	RPELELWRLRSRWRPLGVPRRCHRRNWKEPVR AQPLSVTVWAPRCQRP/QPPAPEPSSPNAA VPEAI PTPRAAASAALELPLGPAPVSVAPQAEAEARSTP GPAGSRLGPETFRQRFRQFRYQDAAGPREAFRQL REL/SPRQWLRPD\RTKEQIVEMLVQEQLLAILP EAARARRRRRTDVRITG
3480	A	117	2226	RRGSRSRGPFAEPAAPGGLCSSSEEKTEEGMAV GLCKAMSQGLVTFRDVALDFSQEEWEWLKPSQ KDLYRDVMLENYRNLVWLGLSISKPNMISLLEQ GKEPVMVERKMSQGHCADWESWWEIEELSPK WFIDEDEISQEMVMERLASHGLECSSFREAWKY KGEFELHQNAERHFMQVTA VKEISTGKRDNEF SN/IWEKHTPEISIFNTTESPTIQQVHKFDIYDKLF PQNSVII EYKRLHAEKESLIGNECEEFNQSTYLSK DIGIPPGEKPYESHDFSKLLSFHSLFTQHQTTHFG KLPHGYDECDAFSCYSFFTQPRIHSGEKPAC NDCGKAFSHDFLSEHQRTTHIGEKPYECKECNKA FRQSAHLAQHQRIHTGEKPFACNECGKAFSRYAF LVEHQRIHTGEKPYECKECNKA FRQSAHLNQH RIHTGEKPYECNQCGKAFSRRIALTLHQRIHTGE KPFKCSECGKTFGYRSHLNQHQRHTGEKPYECI KCGKFFRTDSQLNRHHRIHTGERPFECCKGKAF SDALVLIHHRSHAGEKPYECNKCGKAFSCGSY LNQHQRHTGEKPYECSECGKAFHQILSLRLHQRI HAGEKPYKCNESQVRRELA VSRGLTTKPADT GPDSTLNAAKVAEPARAGTEAALRPALSVAES TSLGPLHQRRFPEAPAAHPGGTGFTVCAS
3481	A	2	1522	ASRHGMPGALLMLL GALGPPLAPGVRGSEAE RLREKLFSGYDSSVRPAREVGDVRV SVGLILAQ LISLNEKDEEMSTKVYLDLEWTDYRLSWDPAEH DGIDSLRITAESVWLPDVVLLNNNDGNFDVALDI SVVVSSDGSVRWQPPGIYRSSCSIQVTYFPFDWQ NCTMVFSSYSYDSSEVSLQTGLGPDGQGHQEIHI

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				HEGTFIENGQWENIHKPSRLIQPPGDPRGGREGQ RQEVIFYLHRRKPLFYLVNVIAPCILITLLAIFVFY LPPDAGEKMGLSIFALLTLTVFLLLLADKVPETSL SVPIIKYLMFTMVLVTFSVLSVVVLNLHHRSPH THQMPLWVRQIFIKLPLYLRLKRPKPERDLMPE PPHCSSPGSGWGRGTDEYFIRKPPSDFLFPKPNRF QPELSAPDLRRFIDGPNRAVALLPELREVVSSISYI ARQLQEEDHDALKEDWQFVAMVVDRLFLWTF IIFTSVGT\VFILDATYHLPPDPFP
3482	A	1273	172	ERWDSGGADAEWYALADWTA VWLPRSDFYTR LQTGEGHVPA LR LPAGMPD SPREL VPKQAPCSP SDPALPWTLGHGNQPPAVVPEPQGMPGAGVAA RPGRRFGVYLLYCLNPRYRVR\VYVGFTVNTARR VQQHNGGRKKGGA\GRTSGRGPWEMVLV\VHGF PSSVAALRFEWA WQHPHASRRLAHVGPRLRGET AFAFHLR VLAHMLRAPPWARLPLTLR WVRPDLR QDLCLPPPHVLLAFGPPPAQVPRPQRRRAGPFD DAEPEPDQGDGACCSLCAQTIQDEEGPLCCPHP GCLLRAHVICLAEFLQEPEGQLLPLEGQCPCCE KSLWGDLIWL CQMDTEKEVEDSELEEAHWTD LLET
3483	A	230	3686	WRPWPCIDTSWNLQVAARTLRVSSAQCGLVPT MARVESPVPAARASLTGSCVLGQAMPLRGGAGP SPASHGPTHGPSDPRTCLPGRGAGGMRPHGRGA LGCCGLCSFYTCHGAAGDEIMHQDIVPLCAADIQ DQLKKRFA YLSGGRGQDGSPVITFPDYPAFSEIPD KEFQNVMTYLT SIPS LQDAGIGFILVIDRRRDKW TSVKASVLR IAASFPANLQLVL VLRPTGFFQRTLS DIAFKFNRRDDFKMKVPVIMLSSVPDLHG YIDKSQ LTEDLGGTLDYCHSRWLCQRTAIESFALMVKQT AQMLQSFGT ELAETELPNDVQSTSSVLC AHT EK KDKAKEDLR LALKEGHSVLESLRELQ AEGSEPSV NQDQLDNQATVQRLLAQLNETEA AFDEFWAKH QQKLEQCLQLRHFEQGFREV KAILDAASQKIATF TDIGNSLAHVEHLLRDLANFQEKSGVFVERARA LSLTASSFIGNKHYA VDSIRPKCQELRHLCDQFSA EIARRRGLLSKSLELHRRLETSMKWCDEGIYLLA SQPVDKCQSQDGAEAA LQEIEKFLETGAENKIQE LNAIYKEYESILNQDLMEHVRKV FQKQASMEEV FHRRQASLKKLAARQTRPVQPVAPRPEALAKSP CPSPGIRRGSESSSSEGGALRRGPYRRAKSEMSES RQGRGSAGEEEESLAILRRHVMSELLDTERAYVE ELLCVLEGYAAEMDNPLMAHLLSTGLHNK KDV LFGNMEEIYHFHNRIFLRELENYTDCPELVGRCF LERMEDFQIYEKYCQNKPRSESLWRQSCDCPFFQ ECQRKLDHKLSDSYLLKPVRITKYQLLLKEM LKYSRNCEGAEDLQEALSSILGILKAVNDSMHLI AITGYDGNLGD LGKLLMQGSFSVWTDHKRGHT KVKELARFKPMQRHLFLHEKAVLFCKKRENGE GYEKAPSYSYKQSLNMAAVGITENVKGDAKKFE IWYNAREEVYIVQAPTPEIKAA WVNEIRKVLTSQ LQACREASQHRAL EQSQLPLPAPTSTSPSRGNSR NIKKLEERKTDPLSLEGYVSSAPLTKPPEKGKGW SKTSHSLEAPEDDGGWSSAEEQINSSDAEEDGGL GPKKLVP GKYTVVADHEKGGPDALRVRS GDVV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3484	A	208	6103	ELVQEGDEGLW VTMAQQAADKYLYVDKNFINNPLAQADWAAK KLVWVPSDKSGFEPASLKEEVGEEAIVELVENGK KVKNKDDIQKMNPPKFSKVEDMAELTCLNEAS VLNHLKERYYSGLIYTYSGLFCVVINPYKNLPIYS EEIVEMYKGGKRHEMPPHIYAITDTAYRSMMDQ REDQSILCTGESGAGKTENTKKVIQYLA YVASSH KSKKDQGELERQLQANPILEAFGNAKTVKNDN SSRFGKFIRINFVNGYTVGANIETYLEKSRAIRQ AKEERTFHIFYLLSGAGEHLKTDLLEPYNKYR FLSNGHVTIPGQQDKDMFQETMEAMRIMGPIEEE QMGLLRVISGVLQLGNTVFKKERNTDQASMPDN TAAQKVSHLLGINVTDFTRGILTPRIKVG RDYVQ KAQTKEQADFAIEALAKATYERMFRWLVL RINK ALDKTKRQGASFIGILDIA GFEIFDLNSFEQLCINY TNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFG LDLQPCIDLIEKPAGPPGILALLDEECWFPKATDK SFVEKVMQEQGTHPKFKPKQLKDKADFCIIHY AGKVDYKADEWLMKNMDPLNDNIATLLHQSSD KFVSELWKDVDRIGLDQVAGMSETALPGAFKT RKGMFRTVGQLYKEQLAKLMATLRNTNPNFVR CIIPNHEKKAGKLDPHLVLDQLRCNGVLEGIRICR QGFPNRVVFQEFRQRYEILTPNSIPKGFMDGKQA CVLMIKALELDSNL YRIGQSKVFFRAGVLAHLEE ERDLKITDVIIGFQACCRGYLARKAFARQQQLT AMKVLQRNCAAYLKL RNWQWWRLFTKVKPLL QVSRQEEEMMAKEEELVKVREKQLAAENRLTE METLQSQLMAEKLQLQEQLQAETELCAEAEEELR ARLTAKKQVELEEICHDL EARVEEBEERCQHLQA EKKKMQQNIQEELEEEESARQKLQLEKVT EAKLKKLEEEQIILEDQNC KLAKEKKLEDRIA EF TTNLT EEEESKSLAKLKNKHEAMITDLEERLRR EEKQRQELEKTRRKLEGDSTDLSDQIAELQAQIA ELKMQLAKKEEELQAALARVEEEAAQKNMALK KIRELESQISELQEDLK CERASRNKA EKQKRD LG EELEALKTELED TLDSTAAQQELRSKREQEVN IL KKTLEEEAKTHEAQIQEMRQKHSQAVEELAEQL EQTKRVKANLEKAKQTL ENERGELANEVKVLLQ GKGDSEHKRKKVEAQLQELQVKFNEGERV RTEL ADKVTKLQVELDNVTGLLSQSDSKSSKLT KD FS ALESQ LQDTQELLQEENRQKLSLSTKLKQVEDE KNSVFREQLEEEEEEA KHNLEKQIATLHAQVADM KKKMEDSVGCLETAEEVKRKLQKDLEGLSQRHE EKVAAYDKLEKTKTR LQQELDDLVDLDHQRQ SACNLEKKQKKFDQL LAEEKTISAKYAEERDRA EAEAREKETKALSLARALEEAMEQKAELERLNK QFRTEMEDLMSSKDDVGKSVHELEKSKRAIEQQ VEEMKTQLEEELEDELQATEDAKLRLEVN LQAM KAQFERDLQGRDEQSEKKKQLVRQVREMEAE LEDERKQRSMAVAARKKLEMDLKDLEAHIDS A NKNRDEAIKQLRKLQAQMKDCMRELD DTRASR EEILAQAKENEKKLKSMEAE MIQLQEELAAAE R AKRQAQQRDELADEIANSSGKGALALEEKRR L EARIAQLEEELEEEQGNTE LINDRLKKANLQIDQ I NTDNLNLSHAQKNENARQQLERQNKELKVKL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				QEMEGTVKSKYKASITALEAKIAQLEEQLDNETK ERQAACKQVRRTEKKLKDVLQVDDERRNAEQ YKDQADKASTRLKQLKRQLEEAEAAQRANASR RKLQRELEDA TETADAMNREVSSLKNKLRGDL PFVPPRRMARKGAGDGSDEEVDGKADGAEAKP AE
3485	A	2	1782	CSTGVSKAPLTYLMSYGFELGWRKGNRAVACR EDRGGESVGMQESILSQVHWWEAEPVEKTPGR DSEATIMSLRVHTLPTLLGAVVRPGCRELLCLLM ITVTVGPGASGVCPTACICATDIVSCTNKNLSKVP GNLFRLIKRLDLSYNRIGLLDSEWIPVSFAKLNTL ILRHNNITSISTGSFSTTPNLKCLDLSSNKLKTIVK NAVVFQELKVLEVLLLYNNHISYLDPSAFGGLSQL QKLYLSGNFLTQFPMDLYVGRFKLAELMFLDVS YNRIPSMPMHHINLVP GKQLRGIY LHGNPFVCD CSLVSLLVFWYRRHFSSVMDFKNDYTCRLWSDS RHSRQVLLLQDSFMNCSDSINGSFALGFIHEAQ VGERLMVHCD SKTGNANTDFIWVGPDRLLLEPD KEMENFYVFHNGSLVIESPRFEDAGVYSCIAMNK QRLNETVDVTINVSNTVSRSHAHEAFNTAFTT LAACVASIVLVLLYLYLTPCPCCKTKRQKNML HQSNAHSSILSPGPASDASADERKAGAGKR VVFL EPLKDTAAGQNGKVRLFPSEA VIAEGILKSTRGK SDSDSVNSVFS DTPFVAST
3486	A	357	1173	GDPRETKVFPSPRSFARNTVGVSHHQSHLFHTVSR IYVEDKHKILYCEVPKAGCSNWKRLMVLNGLA SSAYNISHNAVHYGKHLKKLDSFDLKGITYRLDT YTKLVLRDPMERLVS AFRDKFDHPNSYYHPVF GKAIKKYRPNACEEALINGSGVKFKEFIHYLLDS HRPVGMDIHWEKVSKLCYPCLIN YDFVGKFETL EEDANYFLQMIGAPKELKFPNFKDRHSSDERTNA QVVRQYLKDLTRTERQLIYDFYYLDYLMFNYYT PFL
3487	A	2	3281	CDKSGAVPFSTTRSPRRPSRSAGPSLSSVSPRSQ LWASSGLSEEHAAPLLPAWPRHPCPPSLTPGPSM AQGAMRFCSEGDCAISPPRCPRRWLPEGVPVQSP PASMYGSTGSLRRVAGPGPRGRELGRVTAPCTP LRGPPSPRVAPSPWAPSSPTGQPPPGAQSSVIFR FVEKASVRPLNGLPAPGGLSRSWDLGGVSPRPRT PALGPGSNRKLRL EASTSDPLPARGGSALPGSRN LVHGPPAPPQVGADGLYSSLNGLGDPPELATL FGGPADTGFLNQGD TWSSPREVSSHAQRIARAK WEFFYGS LDPPSSGAKPPEQAPSPPGVGSRQGS GVAVGRAAKYSETDLDTVPLRCYRETDIDEVLA EREEADSAIESQPSSEGGPTAYPPAPRPGPLPGP HPSLGSGNEDEDDDEAGGEEDVDDEVFEASEGA RPGSRMPLKSPVPFLPGTSPSADGPDSFSCVFEAI LESHRAKGTSYTSLASLEALASPGPTQSPFFTFEL PPQPPAPRPDPAPAPLAPLEPDSGTSSAADGPWT QRGEEEEAEARAKLAPGREPPSPCHSEDSLGLGA APLGSEPPLSQLVSDSDSELDSTERLALGSTDTLS NGQKADLEAAQRLAKRLYRLDGFRKADVARIHL GKNNDFSKL VAGEYLKFFVFTGMTLDQALRVFL KELALMGETQERERVLAHFSQRYFQCNP EALSSE DGAHTLTALMLLNTDLHGHNIGKRMT CGDFIG

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NLEGLNDGGDFPRELLKALYSSIKNEKLQWAIDE EELRRFLSELADPNPKVIKRISGGSGSGSSPFLDLT PEPGAAVYKHGALVRKVHADPDCKRKTTPRGKRG WKSFGILKGMILYLQKEEYKPGKALSETELKN AJSIHHALATRAS\NYSKRPHVFYLRADWRVFL FQAPSLEQMOSWITRINVVAAMFSAPFPAAVSS QKKFSRPLLPSAATRLSQEEQVTHEAKLKAMA SELREHRAAQLGKKGRGKEAEEQRQKEAYLEFE KSRYSTYAALLRVKLKAGSEELDAVEAALAQAG STEDGLPPSHSSPSLQPKSSQPRAQRHSSEPRPG AGSGRRKP
3488	A	441	1968	GTETPHCWGRGTAGLRRELDREERDGPATMS FPHFGHPYRGAFQFLASASSSTTCCESTLRVSYS VASGSTPAPALCCAPYDSRLLGSARPELGAALGI YGAPYAAAAAQSYPGYLPYSPEPPSLYGALNP QYEFKEAAGSFTSSLAQPGAYYPYERTLGQYQY ERYGAVELSGAGRRKNATRETTSTLKAWLNEHR KNPYPTKGEKIMLAITKMTLTQVSTWTFANARRR LKKENKMTWAPKNKGGEERKAEGGEEDSLGCL TADTKEVTASQEARGLRLSDLEDLEEEEEEEEA EDEEVVATAGDRLTEFRKGAQSLPGCAAAREG RLRRECGLAAPRFSFNDPSGSEEDFLSAETGSP RLTMHYPCLEKPRIWLAHTATASAVEGAPPARP RPRSPECRMIPGQPPASARRLSVPRDSACDESSCI PKAFGNPKFALQGLPLNCAPCRRSEPVVQCQYP SGAEGSGPPAALGVSMQKTPTYRPARQLHTLCH SSLP
3489	A	718	2073	IAAYHKALSYRGHVHANNRGTNNVHFTPPSPS RGILPMNPRNMNHSQVGQIGIPSRTNSMSSSG LGSPNRSSPSIICMPKQQPSRQPFTVNSMSGFGMN RNQAFGMNLSLSSNIFNGTDGSENVTLGLDLSDFP ALADRNRREGSGNPTPLINPLAGRAPHYVGMVTK PANEQSQDFSIHNEDFPALPGSSYKDPTSSNDDSK SNLNTSGKTTSSTDGPKFPGDKSSTQNNNQKK GIQVLPDGRVTNIPQGMVTDQFGMIGLLTFIRAA ETDPGMVHLALGSDLTTLGLNLNSPENLYPKFAS PWASSPCRPQDIDFHPSEYL TNIHIRDKLEFFFS W/TAIKLGRYGEDLLFYLYYMNGGDVLQLLAAV ELFNRDWRYHKEERVWITRAPGMEPTMKTNTY ERGTYFFDCLNWRKVAKFHELYDKLEERPHL PSTFNYNPAQQA
3490	A	2	2833	FVAKMATSQYFDFAQGGGPQYSTQAPTLPLPTV GASYTGQPTPGMDPAVNPAFPAPAGYGGYQP HSGQDFAYGSRPQEPVPTATTMATYQDSYSYGQ SAAARSYEDRPYFQSAALQSGRMTAADSGQPGT QEACGQSPHSGSHSQAPPPQAPIVESGQPASTL SSGYTYPTATGVQPESSASIVTSYPPPSYNPTCTA YTAPSYPNYDASVYSAASPFYPPAQP PPPPPGPPQ QLPPPPAPAGSGSSPRADSKPPLPSKLPRPKAGPR QLQLHYCDICKISCAGPQTYREHLGGQKHKRKE AAQKTGVQPNGSPRGVQAQLHCDLCAVSCTGA DAYAAHIRGSKHQKVFKLHAKLGKPIPTLEPALA TESPPGAEEKPTSPTGPSVCASSRPALAKRPVASK ALCEGPPEPQAAGCRPQWGKPAQPKLEGPGAPT QGGSKAPAGCSDAQPVGPEYVEEVFSDEGRVL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RFHCKLCECSFNLDLNAKDLHVRGRRHRLQYRKK VNPDLPIATEPSSRARKVLEERMQRHLAEERL EQLRRWHAERRRLEEEPPQDVPPHAPPDWAQPL LMGRPESPASAPLQPGRRPASSDDRHVMCKHATI YPTEQELLAVQRAVSHAERALKLVSDTLAEEDR GRREEEGDKRSSVAPQTRVLKGVMRVGILAKGL LLRGDRNVRLALLCSEKPTHSLRRRIAQQPLPRQL QMVTEDYEVSDDPEANIVISSCEEPRMQVTISVT SPLMREDPSTDPGVVEEPQADAGDVLSPKKCLESL AALRHARWFQARASGLQPCVIVIRVLRDLRVRV PTW GALPAWAMELLVEKAVSSAAGPLGPGDAV RRVLECVATGTLTLDGPGQLDPCERDQTDALP MTLQEREDVTASAQHALRMLAFRQTHKVLGMD LLPPRHRLGARFRKRQRGPGEEGEGAGEKKRGR RGGEGLV
3491	A	2	1321	FVGDGALSGCRRGRAPRVPSMAGSLPPCVVDCG TGYTKLGYAGNTEPQFIIPSCIAIRESAKVVDQAQ RRVLRGVDDLDFIGDEAIDKPTYATKWPIRHGII EDWDLMERFMEQVVFVKYLRAEPEDHYFLMTEP PLNTPENREYLAEMFESFNVPGLYIAVQAVLAL AASWTSRQVGERTLTGIVIDSGDGVTHVIPVAEG YVIGSCIKHIPIAGRDITYFIQQLLREREVGIPPEQS LETAKAIKEKYCYICPDIVKEFAKYDVPDPRKWIK QYTGINAINQKKFVIDVGYERFLGPEIFFHPEFAN PDFMESISDVVDEVIQNCPIDVRRPLYKNVVLGSG GSTMFRDFGRRLQRDLKRVVDARLRLSEELSGG RIKPKPVEVQVVTHHMQRYA VWFVGGSMLASTP EFFQVCHTKKDYEYGPSICRHNPNVFGVMS
3492	A	3	2024	PNGVALLHLPAAVIPNTNYMFQDALGGRSRGS REESPAPSRAPASASLWRRLVVVEAKMAAHAAA AAQAAAAQAAHAEAADSWYLALLGFAEHFRTS SPPKIRLCVHCLQAVFPFKPPQRIEARTHLLQLGSV LYHHTKNSEQARSHLEKAWLISQQIPQFEDVKFE AASLLSELYCQENSVDAAKPLLRKAIQISQQTPY WHCRLLFQLAQLHTLEKDLVSACDLLGVGA EY ARVVGSEYTRALFLLSKGMLLLMERKLQEVHPL LTLGQIVENWQGNPIQKESLRVFFLVLQVTHYL DAGQVKSVPCLKQLQQCIQTISTLHDDLEILPSNP ADLFHWLPKEHMCVLVYLVTVMHSMQAGYLE KAQKYTDKALMQLEKLMDCSPILSSFQVILLE HIIMCRLVTGHKATALQEISQVCQLCQSPRLFS NHAAQLHTLLGLYCVSVNCDNAEAQFTTALR LTNHQELWAFIVTNLASVYIREGHRHQEVVLYS LLERINPDHSFPVSSHCLRAAAFYVRGLFSFFQGR YNEAKRFLRETLMKMSNAEDLNRLTACSLVLLGHI FYVLGNHRESNNMVVPAMQLASKIPDMSVQLW SSALLRDLNKACGNAMDAHEAAQMHNFSQQL LQDHIEACSLPEHNLITWTDGPPPVQFQAQNGPN TSLASLL
3493	A	3	2024	PNGVALLHLPAAVIPNTNYMFQDALGGRSRGS REESPAPSRAPASASLWRRLVVVEAKMAAHAAA AAQAAAAQAAHAEAADSWYLALLGFAEHFRTS SPPKIRLCVHCLQAVFPFKPPQRIEARTHLLQLGSV LYHHTKNSEQARSHLEKAWLISQQIPQFEDVKFE AASLLSELYCQENSVDAAKPLLRKAIQISQQTPY

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				WHCRLLFQLAQLHTLEKDLVSACDLLGVGA EY ARVVGSEYTRALFLLSKGMLLLMERKLQEVHPL LTLGGQIVENWQGNPIQKESLRVFFLVLQVTHYL DAGQVKSVPCKLQQLQCCIQTISTLHDEILPSNP ADLFHWLPKEHMCVLYLVTVMHSMQAGYLE KAQKYTDKALMQLEKLMKMLDCSPILSSQVILLE HIIMCRLVTGHKATALQEISQVCQLCQSPRLFS NHAAQLHTLLGLYCVSVN CMDNAEAQFTTALR LTNHQELWAFIVTNLASVYIREG NRHQEVVLYS LLERINPDHSFPVSSHCLRAAFYVRGLFSFFQGR YNEAKRFLRETLKMSNAEDLNRLTACSLVLLGHI FYVLGNHRESNNMVPAMQLASKIPDM SVQLW SSALLRDLN KACGNAMDAHEAAQMHNFSQQL LQDHIEACSLPEHNLITWTDGPPPVQFQAQNGPN TSLASLL
3494	A	2	1615	VLRGQRGPAGGLAEERRRGRNEWRIHDVTTAPF PGLVQRRSRLLIVSQVRYFLKNKVSPDL CNEDGL TALHQCCIDNFEEIVKLLLSHG ANVNAKDNE LW TPLHAAATCGHINLVKILVQYGADLLAVNSDGN MPYDLCEDEPTLDVIETCMAYQGITQEKINEMRV APEQQMIADIHCMIAAGQDLWDIDAQGATLLHI AGANGYLRAAE LLDHGV RVDVKDW D GWEPL HAAAFWGMQMAELLVSHGANLNARTSMDE MPIDLCEEEEFKVLLELKVHKHDVIMKSQLRHK SSLRRTSHRQAS/SVGKVVRRTQPVGTGPNL/YR KEYE/GEEAILWQRSA/AEDQRTSTYNGDIRETR TDQENKDPNPRLEK/PVLLSEFPTKIPRGELDM PV ENGLRAPVSA YQYALANGDVWKVHEVPDYSM AYGNPGVADATPPWSSYKEQSPQTLLELKRORA AAKLLSHPFLLSTHLGSSMARTGESSESGKAPLIG GRTPSYSSNGTSVYYTVTSGDPPLLKFKAPIEEM EEKVHGCCRIS
3495	A	327	1078	APMADTTPNGPQAGAVQFMMTNKLDTAMWL SRLFTVYCSALFVLP LLGLHEAASFYQRALLANA LTSALRLHQRLPHFQLSRAFLAQALLED SCHYLL YSLIFVNSYPVTMSIFPVLLFSLHAATYTKVLA DARG\SNLPLLRL\SVLDKLSANQQN ILKFACNEI FLMPATVFM LFSGQSLLQPFIIYRFLTLRYSSRR NPYCRTL FNELRIVVEHIIMKPACPLFVRRLCLQS IAFISRLAPTVP
3496	A	3	2867	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNA P APGTPAASGWQPPTYHSGRAFSARYPRPSRRGYS SHHGPSWRKKYSLVNRPPGPSDPPADHAVRPLH GARGGQPPVPQQHVLERQVQLSQGQNVVIVKVP PSKSGSASASGAQRGSLEEFEDTPWSDQRPREGE GEPPRGQLQPSRPTARGTCSVEDPLLVCQKEPG KPRMVKSVGSVGDSPREPRRTVSES VIAVKASFP SSALPRTGVALGRKLGSHSVASCAPQLLGDRRV DAGHTDQVPVSGSVGGPARPASGPRQAREASLV VTCRTNKFRKN NYKWVAASSKSPRVARRALSPR VAAENVCKASAGMANKVEKPQLIADPEPKPRKP ATSSKPGSAPSKYKWKASSPSASSSSSFRWQSEA GSKDHASQLSPVLSRSPSGDVRPALAHSGLKPLSG ETPLSA YKVKTRTKIIRRRGSTSLPGDKKSGTSPA ATAKSHLSLRRRQALRGKSSPVLKKT P NKGLVQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VTKHRLCRLPPSRAHLPTKEASSLHAVRTAPTSK VIKTRYRIVKKTPASPLSAPPFLSLPSWRARRLS LSRSLVLNRLRPVASGGGKAQPGSPWWRSGYR CIGGVLYKVSANKLSKTSGQPSDAGSRPLLRTGR LDPAGSCSRSLASRAVQRSLAIRQARQRREKRK EYCMYYNRFGRCNRGERCPYTHDEKVAVCTRF VRGTCKKTDGTCPFSSHVSKEKMPVCSYFLKGI CSNSNCPYSHVYVSRKAEVCSDFLKGYCPLGAK CKKKHTLLCPDFARRGACPRGAQCQLLHRTQKR HSRRAATSPAPGPSDATARSRSASHGPRKPSAS QRPTRQTPSSAALTAATAVAAPPHCPGGSASPS KASSSSSSSSPPASLDHE\APSLQEAALAAACSN RLCKLPFSISLQSSPSGAQPRVRAPRAPLTKDSG KPLHIKPR
3497	A	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCR NLQEFLGGLSPGVLDRLYGHDPATCLAVFREPSL AKNWVMRMLFLEQPLPQAAVALWVKKEFSKA QEESTGLLSGLRIWHTQLLPGLQLLNPFRON LRIALLGGGKAWSDDTSQLGPDKHARDVPSLDK YAEERWEVVLHFMVGSPSAAVSQDLAQLLSQA GLMKSTEPGEPPCITSAGFQFLLLDTPAQLWYFM LQYLQTAQSRGMDLVEILSFLFQLSFTLGKDY VEGMSDSSLNLFQLHLREFGLVFQRKRKSRYY T/RALAINLSSGVSGAGGTVHQPGFIVVETNYRL YAYTESELQIALIALFSEMLYPFPNMVVARVTR ESVQQAIASGITAQQIHFRLTRAHPVMLKQTPVL PPTITDQIRLWELERDLRFTEGVLYNQFLSQVDF ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHS DVKRFWKRQKHSS
3498	A	790	190	RDLGPAALMTASASSFSSSQGVQQPSIYSFSQITR SLFLSNGVAANDKLLSSNRITAIVNASVSGSQRI LRGLQYIKVPVTDARDSRLYDFDPIADLIHTVS MRQGRLLNCMAGMSRSASLCLAYLMKYHSM SLLDAHTWA/TKSRPPIRPNNGFWEQLINYEFK LFNNNTVRMINSPVGNIPDIYEKDLRMISM
3499	A	31	1586	TAGFLAPLEMQRLLTPVKRILQLTRAVQETS PARLLPVAHQRFSTASAVPLAKTDTWPKDVGIL ALEVYFPAQYVDQTDLEKYNNVEAGKYTVGLG QTRMGFCVQEDINSLCLTVVQRLMERIQLPWD SVGRLEVGTETIIDKSKAVKTVLMELFQDSGNTD IEGIDTTNACYGGTASLFNAANWMESSWDGRY AMVVCGLDIAVYPSGNARPTGGAGAVAMLIGPK APLALERGLRGTHMENVDYKPNLASEYPIVD GKLSIQCYLRALDRCYTSYRKKIQNQWKQAGSD RPFTLDDLQYMIHFHTPFCKMVQKSLARLMFND LSASSDTQTSLYKGLEAFGLKLEDYTNKDLD KALLKASQDMFDKKTASLYLSTHNGNMYTSS YGCLASLLSHHSAQELAGSRIGAFSYGSGLAASF FSFRVSQDAAPGSPL\DKLVSSSDLPKRLASRKC VSPEEFTEIMNQREQFYHKVNFSPPGDTNSLPGT WYLERVDEQHRRKYARRPV
3500	A	185	2692	MLPTEVPQSHPGPSALLLQLLLPPTSAFFPNIWS LLAAPGSITHQDLTEEAALNVTQLFLEQPPGPRP PLRLEDLGRLLADDLFAAYFGPGSSRRFRAAL GEVSRANAAQDFLPTSRNDPDLHFDAERLGQGR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ARLVGALRETVVAARALDHTLARQRLGAALHA LQDFYSHSNWVELGEQQPHPLLWPRQELQNL QVADPTCSDCEELSCPRNWLGFLLTSGYFGTHP PKPPGKCESHGGHFDSSSQPPRGINKDSTSPGFS PHHMLHLQAAKLALLASIQAFSLRLSRDGRD RLLDITPASSLSFVLDTTGSMGEEINAAKIQARHL VEQRRGSPMEPVHYVLVPFHDPGFGPVFTTSDPD SFWQQLNEIHALGGGDEPEMCLSAQLALLHTPP LSDIFVFTDASPKDAFLTNQVESLTQERRCRVTF VTEDTSRVQGRARREILSPLRFEPYKAVALASGG EVIFTKDQHIRDVAIVGESMAALVTLPLDPPVV VPGQPLVFSVDGLLQKITVRIHGDISSFWIKNPAG VSQGGQEEGGGPLGHTRRFGQFWMVTMDPPQT GTWEIQVTAEDTPGVRVQAQTSLDLFLHFIPME DGPHPLGYPLTQPVAGLQTQLLVEVTGLGSRAN PGDPQPHFSHVILRGVPEGAELGQVPLEPVGPPE RGLLAASLSPTLLSTPRPFSLELIGQDAAGRRLHR AAPQPSTVVPVLELSPSGFLAPGSKVPLSLRIA SFSGPQDLDLRTFVNPSFSLTSNLSRAHLELNESA WGRLLWLEVPDAAAPDSVVMVTVTAGGREANPV PPTHAFLRLVSAAPQDRH
3501	A	1245	5815	RRAHPHSRLSPYLSVSRDPYFFVTVSRTILTSA PAPPRRTAPSMGTALLQRGGCFLLCLSLLLGC WAEGLSGLEFPGAEGQWTRFPKWNACCESEMSF QLKTRSARGLVLYFDDEGFCDFLELILTRGGRLQ LSFSIFCAEPATLLADTPVNDGAWHSVRIRQRFR NTTLFIDQVEAKWVEVKSKRRDMTVFSGLFVGG LPPELRAAALKLTLASVREREPFKGWIRDVRVNS SQVLPVDSGEVKLDDEPPNSGGG\SPCEAGEEGE GGVCLNGGVCSVDDQAVCDCSRTGFRGKDCS QEDNNVEGLAHLMMGDQKKEEYIATFKGSEYF CYDLSQNPIQSSSEITLSFKTLQRNGLMLHTGKS ADYVNLALKNGAVSLVINLGSGAFEALVEPVNG KFNDNAWHDVKVTRNLRQHSGIGHAMVTISVD GILTTGYTQEDYTMGLSDDFFYVGGSPSTADLP GSPVSNNFMGCLKEVVYKNNDVRLELSRLAKQ GDPKMKIHGVVAFKCNVATLDPITFETPESFISL PKWNAKKTGSISFDFRTTEPNGLILFSHGKPRHQ KDAKHPQMIKVDFFAIEMLDGHLYLLLDMGSGT IKIKALLKKVNDGEWYHVDQFQDGRSGTISVNT LRTPTYAPGESEILDDELYLGGLPENKAGLVF PTEVWTALLNYGYVGCIRDLFIDGQSKDIRQMA EVQSTAGVKPSCSKETAKPCLSNPCKNNGMCRD GWNRYVDCSGTGYLGRSCREATVLSYDGSM FMKIQLPVVMHTEAEDVSLRFRSQRAYGILMAT TSRDSADTLRELDAGRVLTVNLDCIRINCNSS KGPETLFAGYNLNDNEWHTVRVVRGKSLKLT VDDQQAMTGQMGADHTRLEFHNIETGIITERRY LSSVPSNFIGHLQSLTFNGMAYIDLCKNGDIDYC ELNARFGFRNIALDPVTFKTKSSYVALATLQAYT SMHLFFQFKTTSLDGLILYNSGDGNDFIVVELVK GYLHYVFDLGNGANLIKSSNKPLNDNQWHNV MISRDTSNLHTVKIDTKITTQITAGARNLDLKS YIGGVAKETYKSLPKLVHAKGFGQCLASVDLN G\RLP\DLISDGSFSCNGTDSRRGMWKGPS\TCQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EDSCSNQGVCLQQWDGFSCDCSMTSFSGLCND PGTTYIFSKGGGQITYKWPNDRPSTRADRLAIGF STVQKEA VLVRVDSSSGLGDYLELHHQKGIGVK FNVGTDIAIEESNAINDGKYHVVRFTSRGGNA TLQVDSWPVIERYPAGRQLTIFNSQA TIHGGKEQ GQPFQGLSGLYYNGLKVLNMAAENDANIAIVG NVRLVGEVPSSMTTESTATAMQSEMSTSIMETTT TLATSTARRGKPPTKEPISQTTDDILVASAECPSD DEDIDPCEPSSGGLANPTRAGGREPYPGSAEVIRE SSSTGMVVGIVAAAALCILLIYAMYKYRNRDE GSYHVDESRYISNSAQSNGA VVKEKQPSSAKSS NKNKKNKDKKEYV
3502	A	394	72	KPAHLPTFTVIIMPKRKPSEGAMSDKVK/AKFELQ RRSAGLFSKPTPPKPTRPKKDPANQRQKLPKVR KKGADA/SKEGNSPAEERCMSVQTQKVEGWRS SELPVALSF
3503	A	43	3358	SGGRGPVVRVSEQLSPSAEQVSQISLGRRLPS SLPPPSRALAPTRAPDTALTIMEVAEVESPLNPS CKIMTFRPSMEEFREFNKYLAYMESKGAHRAGL AKVIPKKEWKPRQCYDDIDNLLIPAPIQQMVTGQ SGLFTQYNIQKKAMTVKEFRQLANSKGYCTPRY LDYEDLERKYWKNLTFVAPIYGADINGSIYDEGV DEWNIARLNTVLDVVEEECGISIEGVNTPYLFG MWKTTFAWHTEDMDLYSINYLHFGEPKSWYAI PEHGKRLERLAQGGFPSSSQGDAFLRHKMTLIS PSVLKKYGIPFDKITQEAGEFMITFPYGYHAGFN HGFNCAESTNFA TVRWIDYGVAKLCTCRKDM VKISMDIFVRKFQPDYQLWKQKDIYTIDHTKP TPASTPEVKA WLQRRRKVRKASRSFQCARSTSK RPKADEEEVSDVDGAEPNPDSVTDDLK VSE KSEAAVKLRNTEASSEEESASRMQVEQNLS DHI KLSGNSCLSTS VTEDIKTEDDKA YAYRSVPSISSE ADDSIPLSTGYEKPEKSDPSELSWPKSPESCSSVA ESNGVLTEGEESDVESHGNGLEPGEIPA VPSGER NSFKVPSIAEGENKTSKSWRHPLSRPPARSPMTL VKQQA PSDEELPEVLSIEEEVEETESWAKPLIHL WQTKPPNFAAEQY NATVARMKPHCAICTLLMP YHKPDSSNEENDARWETKLDEVVTSEGKTKPLIP EMCFIYSEENIEYSPN AFLIEDGTSL LISCACCC VRVHASCYGIPSHEICDGLCARCKRNAWTAEC CLCNLRGGALKQTKNNKWAHVMC AVAVEVR FTNVPERTQIDVGRIPQLRLKLCIFCRHRVKRVS GACIQCSYGRCPASFHVTC AHAAGVLM EPDDW PYVVNITCFRHKVNPVNKSKACEKVISVGQTVIT KHNTRYYSRCRVMAVTSQTFYEV MFDDGSFSRD TFPEDIVSRDCLKLGPPEGEVVQVKWPDGKLY GAKYFGSNIAHMYQVEFEDGSQIAMKREDIYTL DEELPKRVKARFVSAGRCHLGTCQVNSLSSPHVS QAQQETYLGFWINSKKSQCNI FLSGTY
3504	A	1124	139	RGEEQFDAEFRFACLGFGERLQEF SRLRAVHR SRAWTCYLAIRMLMATCCPSPTTTACTGPWQRA PPLRLVQKREADSSGLAFASNSLQRRKGLLLR PVAPLRTRPPLLSLPQDFRQVSSVIDVDLLPETH RRVRLHKHGS DRPLGFYIRDGMSVRVAPQGLER VPGIFISRLVRGG LAESTGLLA VSDEILEVNGIEV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				AGKTLNQVTDMMVANSHNLIVTVKPANQRNN VVRGASGRLTGPPSAGPGAEPDSDDDSSDLVIE NRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPS LDDQEQAASSGWGSRIRGDGSGFSL
3505	A	3	2898	SCRSATSQSGCGGGRSWLCSSLKMAAQPPRGIRL SALCPKFLHTNSTSHTWPFSAVAELIDNAYDPDV NAKQIWIDKTVINDHICLTFTDNGNGMTSDKLH KMLSFGFSKDKVTMNGHVPVGLYGNGFKSGSMR LGKDAIVFTKNGESMSVGLLSQTYLAEVIKAEHV VVPVAFNKHQRQMINLAESKASLAAILHSLFSTE QKLLAELDAIIGKKGTRIHWNLRSYKNA TEFD KDKYDIRIPEDLDEITGKKGYKKQERMDQIAPES DYSRLAYCSILYLKPRMQILRGQKVKTKQLVSKS LAYIERDVYRPFKLSKTVRITFGFNCRNKDHYGI MMYHRNRLIKAYEKVGCQLRANNMGVGVVGII ECNFLKPTHNKQDFDYTNEYRLTITALGEKLN YWNEMKVKKNTHEYPLNLPVEDIQKRPDQTVVQ CDACKWRKLPDGMQLPEKWYCSNPNPDPQFR NCEVPEEPEDEDLVHPTYEKTYKKTNKEKFRIRQ PEMIPRINAELLFRPTALSTPSFSSPKESVSKR/RH LSEGTNSYATRLLNNHQVPPQSEPESSNLKRRLS TRSSILNAKNRRLASSQFENSVMYKGDDEDEDVII LEENSTPKPAVDHIDMKSEQSHVEQGGVQVEF VGDSEPCGQTGSTSTSSSRCDQNTAATQTEVPS LVVKEETVEDEIDVRNDAVILPSCVEAEAKIHE TQETTDKSADDAGCQLQELRNQLLLVTTEKENY KRQCHMFTDQIKVLQQRILEMNDKYVKKETCH QSTETDAVFLLESINGKSESPDHMVSQYQQALEE IERLKKQCSALQHVKAECSCSNNESKSEMD AVQLDDVFRQLDKCSIERDQYKSEVELLEMEKS QIRSQCEELKTEVEQLKSTNQQTATDVSTSSNIEE SVNHMDGESLKLRLRVNVGQLLAMIVPDLDLQ QVNYDVDVDEILGQVVEQMSEISS
3506	A	2	2120	RPPEAGGRYRAGGRRQAAPSRPPLPSRRRLPQG GRTRRAMDRPAAAAAAGCEGGGGPNPGPAGGR RPPRAAGGATAGSRQPSVETLDSPTGSHVEWCK QLIAATISSQISGSVTSENVSRDYKALRDGNKLA QMEEAPLFPGESIKAIVKDVMYICPFMGA VSGTL TVTDFKLYFKNVERDPHFILDVPLGVISRVEKIGA QSHGDNSCGIEIVCKDMRNRLAYKQEEQSKLG IFENLNKHAFPLSNGQALFAFSYKEKFPINGWKV YDPVSEYKRQGLPNESWKISKINSNYEFCDTYPA IIVVPTSVDKDDLSKVAVFLAKGRVPVLSWIHPE SQATITRCSQPLVGPNDKCKEYKYLQTIMDAN AQSHKLIIFDARQNSVADTNKTKGGGYESESAYP NAELVFLEIHNIHVMRESLRKLKEIVYPSIDEARW LSNVDGTHWLEYIRMLLAGA VRIADKIESGKTSV VVHCSDGWDRTAQLTSLAMLMLDSYYRTIKGFE TLVEKEWISFGHRFALRVGHGNDNHADADRSPIF LQFVDCVWQMTRQFSAFELFLITLDHLYS CLFGTFLCNCEQQRFKEDVYTKTISLWSYINSQL DEFSNPFFVNYENHVLYPVASLSHLELWVNYVY RWNPRMRPQMPIHQNLKELLAVRAELQKRVEG LQREVATRAVSSSSSERGSSPSHFATS VHTLV
3507	A	1	2169	GSSIKIRLTVLCAKNLAKKDFRLPDPFAKIVVD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GSGQCHSTD TVKNTLDPKWNQHYDLYVGKTDSTI TISVWNHKKIHKKQGAGFLGCVRLLSNAISRLKD TGYQRDLCKLNPSTDAVRGQIVVSLQTRDRIG TGGSVVDCRGLLENEGTVYEDSGPGRPLSCFME EPAPYTDSTGAAAGGGNCRFVESPSQDQRLQAQ RLRNPDVVRGSLQTPQNRPHGHQSPELPEGYEQRT TVQGGQVYFLHTQTGVSTWHDPRIPRDLNSVNCD ELGPLPPGWEVRSTVSGRIYFVDHNNRTTQFTDP RLHHIMNHQCQLKEPSQPLPLPSEGSLEDEELPA QRYERDLVQKLKVLRLHLSLQPPQAGHCRIEVS REEIFEESYRQIMKMRPKDLKKRLMVKFRGEEG LDYGGVAREWLYLLCHEMLNPYYGLFQYSTDNI YMLQINPDSSINPDHLSYFHFVGRIMGLAVFHGH YINGGFTVPFYKQLLGKPIQLSDLESVDPELHKS VWILENDITPVLDTFCVEHNAFGRILQHELKPN GRNVPVTEENKKEYVRLYVNWRFMRGIEAQFL ALQKGFNELIPQHLLKPFQKELELIIGGLDKIDL NDWKSNTLRKHCVADSNIWRWFQAVETFDDEE RRARLLQFVTGSTRVPLQGFKALQGSGTGAAGPR LFTIHLIDANTDNLKAHTCFNRIDIPPYESYEKL YEKLLTAVEETCGFAVE
3508	A	3	6388	ILYNPADLGWNPPVSSWIEKREIQTERANLTILF DKYLPCLDTRLRTRFKKIPIPEQSMVQMVCHLLE CLLTEDIPADCPKEIYEHYFVFAAIWAFGGAMV QDQLVDYRAEFKWWLTEFKTVKFPSQGTIFDY YIDPETKKFEPWSKLVPQFEFDPEMPLQACL VHT SETIRVCYFMERLMARQRPVMLVG TAGTGKSVL VGAKLASLDPEAYLVKNVPFNYYTTSAMLQAVL EKPLEKKAGRNYGPPGNKKLIYFIDDMNMPEVD AYGTVQPHITIRQHLDYGHWDYDRSKLSLKEITNV QYVSCMNPTAGSFTINPRLQRHFSVFLSFPDAD ALSSIYSIILTQHLKLGNFPA SLQKSIPPLIDLALAF HQKIATTF LPTGIKFHYIFNL RDFANIFQGILFSSV ECVKSTWDLIRLYLHESNRVYRDKMVEEKDFDL FDKIQTEVLKKTFFDIEDPVEQTQSPNLYCHFAN GIGEPKYPVQSWELLTQTLVEALENHNEVNTV MDLVLFEDAMRHVCHINRILESPRGNALLVGVG GSGKQSLTRLAAFISSMDVFQITLRKGYQIQDFK MDLASLCLKAGVKNLNTVFLMTDAQVADERFL VLINDLLASGEIPDLYSDDEVENIISNVRNEVKSQ GLVDNRENCWKFFIDRIRRLKVTLCFSPVGNKL RVRSRKFPAIVNCTAIHWFHEWPPQALESVSLRF LQNTGIEPTVKQSISKFMAFVHTSVNQTSQSLS NEQRYNYTTPKSFLEFIRLYQSLLRHHRKELCK TERLENGLLKLHSTSAQVDDLKAKLAAQEVELK QKNEDADKLIQVVGVEDKVSREKAMADEEEQ KVA VIMLEV KQKQKDCEEDLAKAEPALTAQA ALNTLNKTNLTELKSFGSPPLAVSNVSAAVMVL MAPRGRVPKDRSWKAAKV TMAKV DGLDSLIN FNKENIHENCLKAIRPYLQDPEFNPEFVATKSYA AAGLCSWVINIVRFYEVFCDVEPKRQALNKA TA DLTAAQEKLA AIKAKIAHLNENLAKLTARFEKA TADKLKCQQA EAVTAVTISLANRLVGGLASENV RWADAVQNFKQQERTLCGDILLITAFISYLGFFT KKYRQSLLDRTWRPYLSQLKTPIPVTPALDPLRM

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				<p>LMDDADVAAWQNEGLPADRMSVENATILNCE RWPLMVDPQLQGIKWKNKYGEDLRVTQIGQKG YLQIEQALEAGAVVLLENLEESIDPVLGPLLGRE VIKKGRFIKIGDKECEYNPKFRLILHTKLANPHYQ PELQAQATLINFTVTRDGLDQLLA VVSMERP DLEQLKSDLTKQQNGFKITLKTLEDSSLRLSSAS GNFLGETVLVENLEITKQTAAEVEKKVQEAQVT EVKINEAREHYRPAAARASLLYFIMNDLSKIHPM YQFSLKAFSIVFQKAVERAAPDESLRERVANLID SITFSVYQYTIRGLFECDKLTYLAQLTFQILLMNR EVNAVELDFLLRSPVQTGTASPVEFLSHQAWGA VKVLSSMEEFNSLDRDIEGSAKSWKKFVESECE KEKLPQEWKNKTALQRLCMLRAMRPDRMTYAL RDFVEEKLGSKYVVGRALEDFA TSFEESGPATPMF FILSPGVDP LKDVESQGRKLG YTFNNQNFHNVS L CQQQEVVAEALDLAAKKGHWWILQNTLEMCS RETEFKSILFALCYFHAVVAERRKFGPQGWNRSY PFNTGDLTISVNLVYNFLEANAKVPYDDLRYLFG EIMYGGHITDDWDRRLCRTYLGEFIRPEMLEGEL SLAPGFPLPGNMDYNGYHQYIDAEPPESP YLYG LHPNAEIGFLTQSEKLFRTVLELQPRDSQARDG AGATREEKVKALLEEILERV TDEFNIPELMAKVE ERTPYIVVAFQECGRMNIL TREIQRSLRELEGLK GELTMTSHMENLQNALYFDMVPESWARRAYPS TAGLAAWFPDLLNRIKELEAWTGDFTMPSTVWL TGFFNPQSFLTAIMQSTARKNEWPLDQMALQCD MTKKNREEFRSPREGAYIHGLFMEGACWDTQA GIITEAKLKD LTPMPVMFIKAIPADIRQDCGHVY SCPVTKTSQRDPTYVWTFNLKTKENPSKWVLA GVALLQI</p>
3509	A	3	6388	<p>ILYNPADLGWNPPVSSWIEKREIQTERANLTILF DKYLPTCLD LTRFRKKIPIEQSMVQM VCHLLE CLLTTEDIPADCPKEIYEHYFVFAIWAFFGAMV QDQLVDYRAEFKWWLTEFKTVKFPSQGTIFYD YIDPETKKFEPWSKLV PQFEFDPEMPLQACLVHT SETIRVCYFMERLMARQRPVMLVGTAGTGKSVL VGAKLASLDPEAYLVKNVPFNYTTSAMLQAVL EKPLEKKAGRNYGPPGNKKLIYFIDDMNMPEVD AYGTVQPHTIIRQHLDYGHWYDRSKLSLKEITNV QYVSCMNPTAGSFTINPRLQRHFSVFLSFPGAD ALSSIYSIILTQHLLKGNFPASLQKSIPPLIDLALAF HQKIATTF LPTGIKFHYIFNLRDFANIFQGILFSSV ECVKSTWDLIRLYLHESNRVYRDKMVEEKDFDL FDKIQTEVLKKT FDDIEDPVEQTQSPNLYCHFAN GIGEPKYMPVQSWELLTQTLVEALENHNEVNTV MDLVLFEDAMRHVCHINRILESPRGNALLVGVG GSGKQSLTRLAAFISSMDVFQITLRKGYQIQDFK MDLASLCLKAGVKNLNTVFLMTDAQVADERFL VLINDLLASGEIPDLYSDDEVENIISNVRNEVKSQ GLVDNRENCWKFFIDRJRRLKVTLCFSPVGNKL RVRSRKFPAINCTAIHWFHEWPQQALESVSLRF LQNTGIEPTVKQSISKMAFVHTSVNQTSQSYLS NEQRYNYTTPKSFLEFIRLYQSLLHRHRKELKCK TERLENGLLKLHSTSAQVDDLKAKLAAQEVELK QKNEDADKLIQVVG VETDKVSREKAMADEEEQ</p>

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KVAVIMLEVKKQKQDCEEDLAKAEPALTAQA ALNTLNKTNLTELKSFSGPPLAVSNVSAAVMVL MAPRGRVPKDRSWKAAKVMAKVDGFLDSLIN FNKENIHENCLKAIRPYLQDPEFNPEFVATKSYA AAGLCSWVINIVRFYEVFCDVEPKRQALNKATA DLTAQEKLAIAKAKIAHLNENLAKLTARFEKA TADKLKCCQEAETAVTISLANRLVGGLASENV RWADAVQNFKKQERTLCGDILLITAFISYLGFFT KKYRQSLLDRTWRPYLSQLKTPIPVTPALDPLRM LMDDADVAAWQNEGLPADRMSSVENATILINCE RWPLMVDPQLQGIKWINKYGEDLRVTQIGQKG YLQIEQALEAGAVLIENLEESIDPVLGPLLGRE VIKKGRFIKIGDKECEYNPKFRLILHTKLANPHYQ PELQAQATLINFTVTRDGLDQLLAADVSMERP DLEQLKSDLTKQONGFKITLKTLEDSSLRLSSAS GNFLGETVLVENLEITKQTAAEVEKKVQEAKVT EVKINEAREHYRPAAARASLLYFIMNDLSKIHMP YQFSLKAFSIVFQKAVERAAPDESLRERVANLID SITFSVYQYTIRGLFECDKLTYLAQLTFQILLMNR EVNAVELDFLLRSPVQTGTASPVEFLSHQAWGA VKVLSSMEEFNSLDRDIEGSAKSWKKFVESECE KEKLPQEWKNKTALQRLCMLRAMRPDRMTYAL RDFVEEKLGSKYVVGRAIDFATSFEESGPATPMF FILSPGVDPLKDVESQGRKLGTYFNNQNFHNVS LGGQEVVAEALDLAAKKGHVILQNTLEMCS RETEFKSILFALCYFHAVVAERRKFGPGWNRSY PFNTGDLTISVNVLYNFLEANAKVPYDDLRYLFG EIMYGGHITDDWDRRLCRTYLGEFIRPEMLEGEL SLAPGFPLPGNMDYNGYHQYIDAELPPSPYLYG LHPNAEIGFLTQTSEKLFRTVLELQPRDSQARDG AGATREEKVKALLEEILERVTFDEFNIPELMAKVE ERTPYIVVAFQECGRMNILTREIQRSLRELEGLK GELTMTSHMENLQNALYFDMVPESWARRAYPS TAGLAAWFPDLLNRIKELEAWTGDTMPSTVWL TGFFNPQSFLTAIMQSTARKNEWPLDQMALQCD MTKKNREEFRSPREGAYIHGLFMEGACWDTQA GIITEAKLKDLPMPVPMFIKAIPAD\RQDCGHVY SCPVTKTSQRDPTYVWTFNLKTENPSKWVLA GVALLQI
3510	A	390	3330	AAGSGSRPPAPAARKMADLAECNIKVMCRFRPL NESEVNRGDKYIAKFQGEDTVVIASKPYAFDRV QSSTSQEQVYNDCAKKIVKDVLEGYNITIFAYG QTSSGKTHTMEGKLHDPEGMGIIIPRIVQDIFNYI SMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLSV HEDKNRVPYVKGCTERFVCSPDEVMDTIDEGKS NRHVAVTNMNEHSSRSHSIFLINVKQENTQTEQK LSGKLYLVDLAGSEKVSKTGAEGAVLDEAKNIN KLSALGNVISALAEGSTYVPYRDSKMTRILQDS LGGNCRTTIVICCPSSSYNESETKSTLLFGQRAKTI KNTVCVNVELTAEQWKKKYEKEKEKNILRNTI QWLENELNRWRNGETVPIDEQFDKEKANLEAFT VDKDITLTNDKPATAIGVIGNFTDAERRKCEEIA KLYKQLDDKDEEINQSSQLVEKLKTQMLDQEEL LASTRRDQDNMQAELNRLQAENDASKEEVKEV LQALEELAVNYDQKSQEVEDKTKEYELLSDELN

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				QKSATLASIDAELQKLKEMTNHQKKRAAEMMA SLLKDIAEIGIAVGNNDVKQPEGTGMIDEEFTVA RLYISKMKSEVKTMTVKRCKQLESTQTESNKKME ENEKELAACQLRISQHEAKIKSLTEYLQNVEQKK RQLEESVDALSEELVQLRAQEKVHEMEKEHLNK VQTANEVKQAVEQQIQSHRETHQKQISSLRDEVE AKAKLITDLQDNQKMMLEQERLRVEHEKLKA TDQEKSRKLHELTVMQDRREQARQDLKGLEETV AKELQTLHNLRLKLFVQDLATRVKKSAEIDSDDT GGSAAQKQKISFLENNLEQLTKSAQTSWYRDNA DLRCELPKLEKRLRATAERVKALESALKEAKEN ASRDRKRYQQEVDRIKEAVRSKNMARRGHSAQI AKPIRPGQHPAASPTHPSAIRGGGAFVQNSQPVA VRGGGGKQV
3511	A	1	1757	MASVQASRRQWCYLCDLPKMPWAMVWDFSEA VCRGCVNFEGADRIELLIDAAARQLKRSHVLPEGR SPGPPALKHPATKDLAAAAAQGPQLPPPQAQPQP SGTGGGVSGQDRYDRATSSGRLPLPSPALEYTLG SRLANGLGREEA VAEGARRALLGSMPLMPPGL LAAAVSGLGSRGLTLAPGLSPARPLFGSDFEKEK QORNADCLAELEAMRGRAEEWHGRPKAVREQ LLALSACAPFNVRFKKDHGLVGRVFAFDATEARP PGYEFELKLFTEYPCGSGNVYAGVLAVARQMFH DALREPGKALASSGFKYLEYERRHSGGEWRQLG ELLTDGVRSFREPAEALPQQYPEPAPAALCGP PPRAPSRLNAPTPTRRRKASPEPEGEAAGKMTTEE QQQRHWVAPGGPYSAETPGVPSPIAALKNVAEA LGHSPKDPGGGGGPVRAGGASPAASSTAQPPTQ HRLVARNGEAEVSPTAGAEAVSGGGSGTGATPG APLCCTLCRERLEDTHFVQCPPVPEHKFCFPCSR KFIKAQGPAGEVYCPSGDKCPLVGSSVPWAFMQ GEIATILAGDIKVKKERDP
3512	A	3	1994	NTNSSSVTNSAAGVEDLNIVQVTPDNEKERLSS IEKIKQLREQVNDLFSRKFGAIGVDFPVKVPYR KITFNPGCVIDGMPPGVVFKAPGYLEISSMRRL EAAEFIKFTVIRPLPGLLSNGEYSTVGKRKIDQE GRVFQEK WERA YFFVEVQNISTCLICKRSMSVSK EYNLRRHYQTNHSHYDQYMERMRDEKLHELK KGLRKYLLGLSDTECPQKQVFANPSPTQKSPVQ PVEDLAGNLWEKLREKRSFVAYSIAIDEITDINN TTQLAIFIRGVDFVSEELDTVPMTGTKSGN EIFSRVEKSLKNFCINWSKLVSASTGTTPMVDA NNGLVTKLSRVATFCKGAELKSICCIHPESLCA QKLKMDHVM DVVVKSVNWICSRGLNHSEFTTL LYELDSQYGSLLYYTEIKWLSRGLVLKRFFESLE EIDSFMSRSGKPLPQLSSIDWIRDLAFLVDMTMH LNALNISLQGHSSQIVTQMYDLIRAFKLCLWET HLTRNNLAHFPTLKLVS RNESDGLNYIPKIAELK TEFQKRLSDFKLYESELTFSSPFSTKIDSVHEELQ MEVIDLQCNTVLKTKYDKVGIFEYFYKLWGSYP KYKHHCAKILSMFGSTYICEQLFSIMKLSKTKYC SQLKDSQWDSVLHIAT
3513	A	1836	513	FKSLLSVKWFCSILVLIFLGTRCYWEMTQSRPSP DPHRGRWEGGRSRPKGGEEGRRRTRVPGLVTAS GPGNPLPDLRGEMAGGRHRRVVGTLHLLLVAA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LPWASRGVSPSASA WPEEKNYHQPAILNSSLARQ IAEGTSISEMWQNDLQPLLIERYPGSPGSAARQ HIMQRIQRLQADWVLEIDTFLSQTPYGYRSFSNII STLNPTAKRHLVLACHYDSKYFSHWNNRVFVG ATDSAVPCAMMLELARALDKLLSLKTVSDSKP DLSLQLIFFDGEEAFLHWSPQDSLYGSRHLAAKM ASTPHPPGARGTSQLHGMDLLVLLDLIGAPNPTF PNFFPNSARWFERLQAIEHELHELGLLKDHSLG RYFQNYSYGGVIQDDHIPFLRRGVPVLHLIPSPFP EVWHTMDDNEENLDESTIDNLNKILQVFVLEYL HL
3514	A	1836	513	FKSLLSVKWFCFSILVLIFLGTRCYWEMTQSRPSP DPHRGRWEGGRSRPKGGEEGRRRTRVPLVTAS GPGNPLPDRLGEMAGGRHRRVVGTLHLLLVAA LPWASRGVSPSASA WPEEKNYHQPAILNSSLARQ IAEGTSISEMWQNDLQPLLIERYPGSPGSAARQ HIMQRIQRLQADWVLEIDTFLSQTPYGYRSFSNII STLNPTAKRHLVLACHYDSKYFSHWNNRVFVG ATDSAVPCAMMLELARALDKLLSLKTVSDSKP DLSLQLIFFDGEEAFLHWSPQDSLYGSRHLAAKM ASTPHPPGARGTSQLHGMDLLVLLDLIGAPNPTF PNFFPNSARWFERLQAIEHELHELGLLKDHSLG RYFQNYSYGGVIQDDHIPFLRRGVPVLHLIPSPFP EVWHTMDDNEENLDESTIDNLNKILQVFVLEYL HL
3515	A	114	754	LCRDLTMTSSKRTKTKTKRPPQRATSNVFAMF DQSQIQEFKEAFNMIDQNRDGFIDKEDLHDMLAS LGKNPTDEYLDAMMNEAPGPINFMTFLTMFGEK LNGTDPEDVIRNAFACFDEEATGTIQEDYLRELL TTMGDRFTDEVEDELYREAPNDKKGIFNYNE FTRHLETGGPKDKDDRKITFQIPSPNVPWLATFG VFLEIFLLHGP
3516	A	1	5169	MAAAPSALLLLPPFPVLSTYRLQSRSRPSAPETDD SRVGGIMRGEKNYYFRGAAGDHGSCPTTTSPLA SALLMPSEAVSSSWSESGLGSGGDEEDTRLLQL LRTARDPSEAFQALQAALPRRGGRGFGPRRKEAL YRALGRVLVEGGSDEKRLCLQLLSDVLRGQGEA GQLEEAFLSALLPQLVVSLEENPALRKDALQIL HICLKRSPEGVLRTLIQGLESTDARLRASTALLL PILLTTEDLLLGLDLTEVIISLARKLGDQETEESE TAFSALQQIGERLGQDRFQSYISRLPSALRRHYN RRLESQFGSQVPYYLELEASGFPEPLPCA VTLS NSNLKFGIIPQELHSRLLDQEDYKNRTQAVEELK QVLGKFNPSSTPHSSLVGFISLLYNLLDDSNFKVV HGTLEVHLHLLVIRLGEQVQQLGVPVIAASVKVLA DNKLVIKQEYMKIFLKLMEVGPQQVLCLELH LKHKHSRVREEVVICISLLTYPSEDFDLPKLSF DLAPALVDSKRRVRQAALFAVLASSMGSGKT SILFKAVDTVELQDNGDGMNAVQARLARKTLP RLTEQGFVEYAVLMPSSAGGRSNHLAHGADTD WLLAGNRTQSAHCHCGDHVRDSMHYGSYPTI CTRRVLSAGKGKNKLPWENEQPGIMGENQTSTS KDIEQFSTYDFIPSAKLKLSQGMFVNDDLCFSRK RVSRNLFQNSRDFNPDCLPLCAAGTTGTHQTNLS GKCAQLGFSQICGKTGSVGSDDLQFLGTTSSHQEK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VYASLNFGSKTQQTFGSQTECTSSNGQNPSPGAY ILPSYPVSSPRTSPKHTSPLIISPCKSQDNSVNFNS WPLKSFEGLSKPKSHRRSLSAQKSSDPTGRNHG \ENSQEKPP\VQLTPAL\VRSPSSRRGLNGTKPVPI PRGISLLPDKADLSTVGHKKKEPDDIWCKEKS LPIDLSELNFKDKDLQDEMHSSLRSLRNSAAK RAKLSGSTSDLESPDSAMKLDLTMDSPSLSSSPNI NSYSESGVYSQESLTSSLSTTPQGKRIMSDIFPTFG SKPCPTLSSAKKKISHIAEQSPSAGSSSNPQQISS FDFTTTKALSEDSVVVVVGKGVFGSLSSAPATCSQ SVISSVENGDTFSIKQSIIEPPSGIYGRSVQQNISSYL DVENEKDAKVSISKSTYNKMRQKRKEEKELFHN KDCEKKEKNSWERMRTGTGTEKMASESETPTGAI SQYKERMPSVTHSPEIMDLSELRFPSKPEIALTEA LRLLADEDWEKKIEGLNFIRCLAAPHSEILNTKL HETNFVAVQEVKNLRSGVSRAAVVCLSDLFTYL KKSMDQELDTTVKVLHKGESNTFIREVDKA LRAMVNNVTPARAVVSLINGGQRYGRKMLFF MMCHPNFEKMLEKYVPSKDLPIKDSVRNLQKQ GLGEIPLDTPSAKGRSHTGSGVGNTRSSSVSRDA FNSAERAVTEVREVTNRKSVPRNSLEAEYLKLIT GLLNAKDFRDRINGIKQLLSDTENNQDLVVGNI KIFDAFKSRLHDSNSKVNLALETMHKMIPLLRD HLSPIINMLIPAIVDNNLNSKNPGIYAAATNVVQA LSQHVNDNYLLQPCTKAQFLNGKAKQDMTEKL ADIVTEL YQRKPHATEQKVLVVLWHLGNMTN SGSLPGAGGNIRTATAKLSKALFAQMGNLLNQ AASQPPHIKKSLEELLDMTILNEL
3517	A	1449	252	QDLKPVLDREYLAIYLMVFFTCNACGESVKKI QVEKHVSVCRNCECLSCIDCGKDFWGGDYKNH VKCISEDQYGGKGY/EKVKTHKGD/ASKQQA WIKISELIK\RPNVSPKVRELLEQISAFDNVPQ/KK AKFQNWMMKNSLKVNESILDQVWNIFSEASNSE PVNKEQDQRPLHPVANPHAEISTKVPASKVKDA VEQQGEVKKNKRRERKEERQKKRKREKKELKLE NHQENSRNQPKKRKKGQADLEAGGEEVPEA NGSAGKRSKKKKQRKDSASEEEARVGAGKRKR RHSKVETDSKKKKMKLPEHPEGGEPEDEAPAK GKFNWKGTIKAILKQAPDNEITIKLRKKVLAQY YTVTDEHHRSEEELLVIFNKKISKNPFTKLLKDK VKLVK
3518	A	3	635	APDSNARNDFHDACSLRVQAGLSSAGPALGNSG LAALMASPSKAVIVPGNGGGDVTHGWYGWVK KELEKIPGFQCLAKNMPDPITARESIWLPFME TELHCDEKTIIGHSSGAIAAMRYAETHRVYAI VLVSA YTSDLGDENERASGYFTRPWQWEKIK ANCPYTV QFGSTDDPFLPWKEQEQEVAD\SW KPNCNTSLTV ATFRTQSFMN
3519	A	81	2277	VRETRREMAMAMSDSGASRLRRQLESGGFEARL YVKQLSQSDGDRDLQEHQRQIALAEETAQNL KRNYYQNYRQFIETAREISYLESEMYQLSHLLTE QKSSLESIPLTLLPAAAAAGAAAAAGGEEGVGGA GGRDHLRGQAGFFSTPGGASRDGSGPGEEGKQR TLTTLLEKVEGCRHLLTPGQYLVYNGDLVEYD ADHMAQLQRVHGFLMNDCLLVATWLPQRRGM

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				YRYNALYSLDGLAVVNVKDNPPMKDMFKLLMF PENRIFQAENAKIKREWLEVLEDTKRALSEKRRR EQEEAAAPRGPPQVTSKATNPFEDDEEEPAVPE VEEEKVDLSMEWQELPEDLDVCIAQRDFEGAV DLLDKLNHYLEDKPSPPVKELRAKVEERVRL TEVLVFELSPDRSLRGPKATRRRAVSQIRLGQC TKACELFLRNRAAAVHTAIRQLRIEGATLLYHK LCHVFFTSLLETAREFEIDFAGTDSGCYSAFVW ARSAMGMFVDAFSKQVFDSKESLSTAAECVKVA KEHCQQLGDIGLDLTFIHALLVKDIQGALHSYK EIIIEATKHRNSEEMWRRMNLMTPEALGKLKEE MKSCGVSNEFYTGDDCWVNLSTVVAFTKQT MGFLLEEALKLYFPELHMVLLESVLEILVAVQHV DYSLRCEQDPEKKAFIRQNASFLYETVLPVVEK RFEEGVGKPAKQLQDLRNASRLIRVNPESTTSVV
3520	A	1706	540	FVAHLAWPWRADGDMEDGVLNEGFLVKGRIHV HNWKARWFILRQNTLVYYKLEGGRRVTPPKGRI LLDGCTITCPCLEYENRPLLIKLTQTSTEFLEA CSREE/RRDAWAFENITGAIHAGQARGKVQQLHS LRNSFKLPPHISLHRIVDKMHDSNTGIRSSPNMEQ GSTYKKTFLGSSLVDWLISNFTASRLEAVTLAS MLMEENFLRPVGVRSMGAIRSGDLAEQFLDDST ALYTFAESYKKKISPKEEISLSTVELSGTVVKQGY LAKQGHKRKNWKVRRFVLRKDPALHYDPSK EENRPVGGFSLRGSLSVALEDNGVPTGVKGNVQ GNLFKVITK\DDTHYYIQA\SSKAE\RAE\WIGSL KSLNMNKDPEGTPDSLPSLPR
3521	A	3	3063	HASVSLSLGCPRPCADTPGPQPQPMDLRVGQRP VEPPPEPTLLALQRPQRLHHHLFLAGLQQRSVE PMRVKMELPACGATLSLVPSLPAFSIPRHQSST PCPFLGCRPCQLSMDTPMPELQEAPEQELRQL LHKDKSKRSAVASSVVKQKLAEVILKKQQAAL RTVHPNSPGIPYRTLEPLETEGATRSMLSSFLPPV PSLPSDPPEHFPLRKTVSEPNLKLRYKPKSLERR KNPLLRKESAPSLRRRAETLGDSSPSSSTPAS GCSSPNDSEHGPNPILGSEALLGQRLRLQETSVAP FALPTVSLLPAITLGLPAPARADSDRRTHPTLGR GPILGSPHTPLFLPHGLEPEAGGTLPRLQPIILLD PSGSHAPLLTVPGLPLPFHFAQSLMTTERLSGSG LHWPLSRTRSEPLPPSATAPPPGPMQPRLEQLKT HVQVIKRSAPSEKPLRLRQIPSAEDLETGDDGGP QVVDGLEHRELGHGQPEARGPAPLQHPQVLL WEQQRLAGRLPRGSTGDTVLLPLAQGGHRLPSR AQSSPAAPASLSAPEPASQARVLSSETPARTLPF TTGLIYDSVMLKHQCSCGDNHRHPEHAGRIQSIW SRLQERGLRSQCECLGRKASLEELQSVHSERHV LLYGTNPLSRLKLDNGKLAGLLAQRMFVMLPCG GVGVDDTDIWNELHSSNAARWAAGSVTDLAFK VASRELKNGFAVVRPPGHHADHSTAMGFCFFNS VALACRQLQQQSKASKILVDWDVHHGNGTQQT FYQDPSVLYISLHRHDDGNFFPGSGAVDEVGAGS GEGFNVNVAWAGGLDPPMGDPEYLAAFRIVVM PIAREFSPDLVLVSAGFDAEAGHPAPLGGYHVS KCFGYMTQQLMNLAGGAVVLALEGGHDLTAIC DASEACVAALLGNRVDP LSEEGWKQKPNLNIR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SLEAIVIRVHSKYWGCMQRLASCPDSWVPRVPG ADKEEVEAVTALASLSVGILAEADRPSEQLVEEEE PMNL
3522	A	9	602	KMAALGEPVRLERDICALLEKLRSGEVPPQ KLQALQRLQSEFCNAVREVEHYETVDISSP EVRANATAKATVAFAASEGHSHPRVVELPKTE EGLGFNIMGGKEQNSPIYISRIIP/GGIADRHGGLK RGDQLLSVNGVSVEGEHHEKAVELLKAAQGV KLVVRYTPKVLEEMESRFEKMRSARRRQQT
3523	A	645	1465	IMAETSLLEAGASAASTAAALNLQVEASCSVCL EYLKEPVIIECGHNFCKACITRWEDLERDFPCP VCRKTSRYRSLRPNRQLGSMVEIAKQLRPSSGRS GMRASAPQHHEALSLFCYEDQEA VCLICAISHTH RAHTV VPLDDATQEYKEKLQKCLEALNQKLQEI TRCKSSEKKPGELKRLVESRRQQLREFEELHRR LDEEQVLLSRLEEEEDILQRLRENAHLGDKR RDLAHLAAEVEGKCLQSGFEMLKVRPLPLHSPS G
3524	A	3	698	PMVRHEAGEALGAIGDPEVLEILKQYSSDPVIEV AETCQLAVRRLEWLQHHGGEPAAGPYLSVDPAP PAER/DVGRLREALDESRLPFERYRAMFALRN AGGEEAALALAEGLHCGSALFRHEVGYYVLGQLQ HEAAVPQLAAALARCTENPMVRHECAEALGAIA RPACLAALQAHADDPERVVRESCKVALDMYEH ETGRAFYADGLEQLRGAPSLGPNPHELPEDS
3525	A	1452	694	EGLQRPEYLVASAAGFQGLAWGGEGRGRAGCS SSGFRDAEPLLLSCPGRNEPLKKERLKWKSDYP MTDGQLRSKRDEFWD TAPAFEGRKEIWDALKA AAYAAEANDHELAQAILDGASITLPHGTLCECY DELGNRYQLPIYCLSPPVNLLLEHTEESLEPPEP PPSVRREFPLK VRLSTGKDVRLSASLPDTVGLK RQLHAQE/GTPKPSWQRWFFSGKLLTDRTRLQET KIQKDFVIQVIINQPPPPQD
3526	A	123	3441	PGNEGLGLAADHNEDLGHLSADAPWPAVTMAP RKRSHHGLGLCCFGGSDIPEINLRDNHPLQFME FSSPINAEELNIRFAELVDELDTDKNREAMFAL PPEKKWQIYCSKKKEQEDPNKLATSWPDYYIDRI NSMAAMQSLYAFDEEETEMRNQVVEDLKTALR TQPMRFVTRFIEGLEGLTCLLNFLRSMDHATCESRI HTSLIGCHIALMNNSQGRAHVLAQPEAISTIAQSL RTENSKTKVAVLEILGAVCLVPGGHKKVQLQAML HYQVYAAERTRFQTLNELDRLGRYRDEVNLK TAIMSFINA VLNAGAGEDNLEFRLHLYEFLMLG IQPVIDKLROHENAILDKHLDFEMVRNEDDLEL ARRFDMVHIDTKSASQMFELIHKKLKYTEAYPC LLSVLHHCLQMPYKRNGGYFQQWQLLDRIQQI VLQDERGVDPDLAPLENFNVKNIVNMLINENEV KQWRDQAEKFRKEHMELVSRLEKEREKETKTL EKEEMMRTL NKMMDKLARESQELRQARGQVA ELVAQLSELSTGPVSSPPPPGGPLTLSSMTTNDL PPPPPLPFACPPPPPPPLPPGGPPTPPGAPPLG MGLPLQDPYPSSDVPLRKKRVQPQSHPLKSFNW VKLNEERVPGTVWNEIDDMQVFRILDLEDPEKM FSAYQRHQELITNPSQQKELGSTEDIYLASRKVK ELSVIDGRRANCIILSKLKSNEEIRQAILKMD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EQEDLAKDMLLEQLLKFIPEKSDIDLLEEHKHEIER MARADRFYEMSRIDHYQQRLQALFFKKKFQER LAEAKPKVEAILLASRELVRSKRLRQMDEVILAI GNFMNKGQGGGAYGFRVASLNKIADTKSSIDRN ISLLHYLIMILEKHFPDILNMPSELQHLPEAAKVN LAELEKEVGNLRRGLRAVEVELEYQRRQVREPS DKFVPVMSDFITVSSFSFSELEDQLNEARDKFAK ALMHFGEHDSKMQPDEFFGIFDTFLQAFSEARQD LEAMRRRKEEEERRARMEAMLKEQRERERWQR QRKVLAAGSSLEEGGEFDDLVSALRSGEVFDKD LCKLKRSRKRSGSQALEVTRERAINRLNY
3527	A	1445	714	LLGTRMLAGQLEARDPKEGTHPEDPCPGAGAV MEKTAVAAEVLTEDCNTGEMPLQQQIIRLHQE LGRQKSLWADVHGKLRSHIDALREQNMELREKL RALQLQRWKARKKSAASPHAGQESHTLALEPAF GKISPLSADEETIPKYAGHKNQSGHSSWGQRSSS NNSAPPKPMSLKIERISSWKTPQENRDKNLSRR RQDRRATPTGRPTPCAERRGVSEDGKVASDTCV TLHWPLGKFRFR
3528	A	484	1777	RISKIQVYYSTGYSSRKMNPTLGLAIFLAVLLTVK GLLKPSFSPRNYKALSEVQGWKQRMAAKELAR QNMDLGFKLLKLAIFYNPGRNIFLSPLSISTAFS MLCLGAQDSTLDEIKQGFNFRKMPEKDLHEGFH YIIHEL TQKTQDLKLSIGNTLFIDQRLQPQRKFLE DAKNFYSAETILT NFQNL EMAQKQINDFI/ESKTH GKINNLIENIDPGTVMLLANYIFFRARWKHEFDP NVTKEEDFFLEKNSSVKVPMFMRSGIYQVGYDD KLSC TLEIPYQKNITAIFILPDEGKLKHLEKGLQV DTFSRWKTLSSRRVVDVSVPRLLHMTGTFDLKKKT LSYIGVSKIFEEHGDLT KIAPHRSLKVGEAVNKA ELKMDERGTGAAGTGAQTLPMETPLVVKIDKP YLLIYSEKIPSVLFLGKIVNPIGK
3529	A	1	5684	VSSVSHENPTEVFEDGENPPSSRSSES GFTEFIQY QADRTDDIDRELSEGQGA AAIPIGSTSSETETAST VGSEETIIQTPSVVTQGTATRSRKTAKTAMQCC LEYVQQFLTRLINLYIIQNNSFSQSLATEHQGD LG REQGETSKWDRNSQGDVKEKNISKQKTSKEYLS AFLAACQLFLECSSFVYIAEGNHTSELRSEKLET DCEHVQPQWLQTLMNACSQASDFS VQSV AISL VMDLVGLTQSVAMVTGENINSVEPAQPLSPNQG RVAVVIRPPLTQGNLRYIAEKTEFFKHVALTLWD QLGDGTPQH HQKSVELFYQLHNLVPSSSICEDVI SQQ LTHKDKKIRMEAHAKFAVLWHLTRDLHINK SSSFVRSFDRSLFIMLDSLNSLDGSTSSVGQAWL NQVLQRHDIARVLEPLLLLLLHPKTQRVSVQRV QAERYWNKSPCYPGEESDKHFMQNFACSNVSQ VQLITSKGNGEKPLTMDEIENFSLTVNPLSDRLSL LSTSETIPMVVSDFDLPDQQIEILQSSDSGCSQSS AGDNLSEYVDPETVNAQEDSQMPKESSPDDDVQ QVVF DLICKVVSGLVESASVTSQLEIEAMPPKC SDIDPDEETIKIEDDSIQQSQNALLSNESSQFLSVS AEGGHECVANGISRNSSPCISGTTHTLHDSVAS IETKSQRSHSSIQFSFKEKLEK VSEKETIVKESG KQPGAKPKVKLARKKDDDKKSSNEK LKQTSV FFSDGLDLENWYSCGEGDISEIESDMGSPGSRKSP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NFNIHPLYQHVLVLYLQLYDSSRTLYAFSAIKAILK TNPIAFVNAISTTSVNNAITPQLSLLQNLLARHRI SVMGKDFYSHIPVDSNHNFRSSMYIELISLCLYY MRSHYPHTVVKVTAQDLIGNRNMQMMSIEILTLL FTELAKVIESSAKGFPSFISDMLSKCKVQKVILHC LLSSIFSAQKWHSEKMAGKNLVAVEEGFSEDLSI NFSEDEFDNGSTLQSLLKVLQRLIVLEHRVM/T IPEE\NETGDFVVS/DLEHISPHQPMSTLQYLHAQ SITCQGMFLCAVIRALHQHCACKMHPQWIGLIT STLPYMGKVLQRVVSVTLQLCRNLDNLQQYK YETGLSDSRPLWMA SIIPDMILTLEGITAIHYC LLDPTTQYHQLLVSDQKHLFEARS GILSILHMI MSSVTLLWSILHQADSSEKMTIAASASLTITNLG ATKNLRQQILELLGPISMNHGVHFM AIAFVWN ERRQNKTTTRTKVIPAASEEQLLVELVRSISVM RAETVIQTVKEVLKQPPAIADKKHLSLEVCM LQFFYAYIQRIPVPNLVDSWASLLILLKDSIQLSLP APGQFLILGVLNEFIMKNPSLENKKDQDRLQDVT HKIVDAIGAIAAGSSLEQTTWLRNLEV KPSPKIM VDGTNLESDVEDMLSPAMETANITPSVYSVHAL TLLSEVLAHLLDMVFYSDEKERVIPLLVNMHYV VPYLRNHSAHNAPSIRACVQLLSSLSGYQYTRR AWKKEAFDLFMDPSFFQMDASCNVNHWRAIMDN LMTHDKTTFRDLMT RVAQA SSSLNLFANRDVE LEQRAMLLKRLAFAIFSS EIDQYQKYL PDIQERLV ESLRLPQVPTLHSQVFLFFRVLLLRMS PQHLTSL WPTMITELVQVFLMEQELTADEDISRTSGPSVA GLETITYTGGNGFSTS YNSQRWLNLYLSACKFLD LALALPSENLPQFQMYRWAFIPEASDDSGLEVRR QGIHQREFKPYVRLAKLLRKRAKKNPEEDNSG RTLGWEPGHLTLTICTVRSMEQLLPFNVLSQVF NSKVTSRCGHSGSPILYSNAFPNKDMKLENHKP CSSKARQKIEEMVEKDFLEGMIKT
3530	A	1	5684	VSSVSHENPTEVFEDGENPPSSRSSES GFTEFIQY QADRTDDIDRELSEGQGA AAIPIGSTSSETETAST VGSEETHIQTPSVVTQGTATRSRKT AQKTAMQCC LEYVQQFLTRLINLYIIQNNSFSQSLATEHQGDLG REQGETSKWDRNSQGDVKEKNISKQKTSKEYLS AFLAACQLFLECSPVYIAEGNHTSEL RSEKLET DCEHVQPPQWLQTLMNAC SQASDFSVQSV AISL VMDLVGLTQSVAMVTGENINSVEPAQPLSPNQG RVAVVIRPPLTQGNLRYIAEKTEFFKHV ALTLWD QLGDGTPQH HQSVELFYQLHNLVPSSSICEDVI SQQLTHKDKKIRMEAHAKFAVL WHLTRDLHINK SSSFVRSFDRSLFIMLSLNSLDGSTSSVGQAWL NQVLQRHDIARVLEPLLLLLLHPKTQRVSVQRV QAERYWNKSPCYPGESDKHFMQNFACSNVSQ VQLITSKGNGEKPLTMDEIENFSLTVNPLSDRLSL LSTSETIPMVVSDFDLDPDQIEILQSSDSGCSQSS AGDNLSEVDPETVNAQEDSQMPKESPDDDVQ QVVFDLICKVVSGLVESASVTSQLEI EAMPPKC SDIDPDEETIKIEDDSIQSQNALLSNESSQFLSVS AEGGHECVANGISRNSSPCISGTTHTLHDSVAS IETKSRQRSHSSIQFSFKEKLSEKVSEKETIVKESG KQPGAKPKVKLARKKDDDKKKSSNEKLKQTSV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				FFSDGLDLENWYSCGEGDISEIESDMGSPGSRKSP NFNHPLYQHVLVLYLQLYDSSRTLYAFSAIKAILK TNPIAFVNAISTTSVNNAITPQLSLLQNLARHRI SVMGKDFYSHIPVDSNHNFRSSMYIEILISLCLYY MRSHYPYTHVKVTAQDLIGNRNMQMMSIEILTLL FTELAKVIESSAKGPFISDMLSKCKVQKVILHC LLSSIFSAQKWHSEKMAKGKLVAVEEGFSEDSLI NFSEDEFDNGSTLQSQLLKVLQRLIVLEHRVMT IPEE\NETGDFVVS\DEHISPHQPMSTLQYLHAQ SITCQGMFLCAVIRALHQHCACKMHPQWIGLIT STLPYMGKVLQRVVSVTLQLCRNLNLIQQYK YETGLSDSRPLWMAIIPDMILTLEGITAIHYC LLDPTTQYHQLLVSVDQKHLFEARSGILSILHMI MSSVTLLWSILHQADSSEKMTIAASALTTINLG ATKNLRQQILELLGPISMNHGVHFMAAIAFVWN ERRQNKTTTRTKVIPAASEEQLLLVELVRSISVM RAETVIQTVKEVLKQPPALAKDKKHLSEVCML QFFYAYIQRIPVPNLVDSWASLLILLKDSIQLSLP APGQFLILGVLNEFIMKNPSLENKKDQDRDQDVT HKIVDAIGAIAAGSSLEQTTWLRNLEVKPSPKIM VDGTNLESDVEDMLSPAMETANITPSVYSVHAL TLLSEVLAHLLDMVFYSDEKERVIPLLVNIMHYV VPYLRNNSAHNAPSRYACVQLLSSLSGYQYTRR AWKKEAFDLFMDPSFFQMDASCNVHWRAIMDN LMTHDKTTFRDLMTRVAVAQSSSLNLFANRDVE LEQRAMLKRLAFAIFSEIDQYQKYLPIQERLV ESLRLPQVPTLHSQVFLFRVLLLRMSPOHLSL WPTMITELVQVFLMEQELTADEDISRTSGPSVA GLETITYTGGNGFSTS YNSQRWLNLYLSACKFLD LALALPSNLQFQMYRWAFIPEASDDSGLEVRR QGIHQREFKPYVVRLAKLLRKRAKKNPEDNSG RTLGWEPGHLTLTICTVRSMEQLLPFFNVLSQVF NSKVTSRCGGHSGSPILYSNAFPNKDMKLENHKP CSSKARQKIEEMVEKDFLEGMIKT
3531	A	553	2470	LISPSALSSQDPALSLKENLEDISGWGLPEARSK ESVSFKDVAVDFTQEEWGQLDSPORALYRDVM LENYQNLLALGPPLHKPDVISHLERGEPPWSMQ REVPRGPCPEWELKAVPSQQQGICKEEPAQEPIM ERPLGGAQAWGRQAGALQRSQAAPGRRTCHG LGRPVEEFPLRCPLFAQQRVPEGGPLLDTRKNV QATEGRTKAPARLCAGENASTPSEPEKFPQVRRQ RGAGAGEGEFVCGECGKAFRQSSSLTLHRRWHS REKAYKCDECGKAFTWSTNLLEHRRHTGKPPF CGECGKAFSCHSSLNHQRHTGERPYKCSACEK AFSCSSLLSMHLRVHTGKPYRCGECGKAFTNR THLTRHHRIHTGKPYQCGSCGKAFTCHSSLT VH EKIHSGDKPFKCS DCEKAFNSRSRLTLHQRTHTG EKPFKCADCGKGFSCHAYLLVHRRHISGEKPFKC NECGKAFSSHAYLIVHRRHTGKPFDCSQCWKA FSCHSSLIVHQRHTGKPYKCECGRAFSQNHCL IKHQKIHSGEKSFKCEKCGEMFNWSSHLTEHQRL HSEKPLAIQFNKHLSTYYVPGSLLGAGDAGLR DVDPIDALDVAKLLCVVPPRAGRNFSLGSKPRN
3532	A	3931	317	HRELQDSPAEPAGSMPLRHWGMARGSKPVGD GAQPMAMGGLKVLLHWAGPGGGEPVWTFSES

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SLTAEVCIHIAHKVGITPPCFNLFALFDAQAQV WLPNNHILEIPRDASLMLYFRHRFYSRNWHGM NPREPAVYRCGPPGTEASSDQTAQGMQLLDPAS FEYLFEGQKHEFVNDVASLWELSTEEIIHHFKNE SLGMAFLHLCHLALRHGIPLEEVAKKTSFKDCIP RSFRRHIRQHSA LTRLRLRN VFRRLRDFQGRLS QQMVMVKYLATLERLAPRFGTERVPVCHLRLLA QAEGEPCYIRDSGVAPTDPGPESAAGPPTHEVLV TGTGGIQWWPVEEEVNKEEGSSGSSGRNPQASL FGKKAKAHKAFGQPADRPREPLGAYFCDFRDT HVGLKEHC VSIHRQDNKCLELSLPSRAAALS FVS LVDGYFRLTADSSHYLCHEVAPPRLVMSIRDGIH GPLLEPFVQAKLRPEDGLYLIHWSTSHPYRLITV AQRSQAPDGMQSLRLRKFPQEQDGA FVLEGWG RSFPSVRELGAALQGCLLRAGDDCFSLRRCLPQ PGETSNLIIMRGARASPRTLNLSQLSFHRVDQKEI TQLSHLGQGTRTNVYEGRLRVEGSGDP EEGKMD DEDPLVPGRDRGQELRVVLKVLDPSHHDIALAF YETASLMSQVSHTHLAFVHGV CVRGPENIMVTE YVEHGPLDVWLRERGRHVPMAWKMMVVAQQLA SALSYLENKNLVHGNVCGRNILLARLGLAEGTSP FIKLSDPGVGLGALSREERVERIPWLAPECLPGG ANSLSTAMDKWGFGATLLEICFDGEAPLQSRSPS EKEHFYQRQHRLPEPSCPQLATLTSQCLTYEPTQ RPSFRITLRLDLTRLQPHNLADVLTVNPDSPASDPT VFHKRYLKKIRDLGEGHFGKVS LYCYDPTNDGT GEMVAVKALKADCGPQHRSGWKQEIDILRTLYH EHIKYKGCCEDQGEKSLQLVMEYVPLGSLRDYL PRHSIGLAQLLLFAQQICEGMAYLHAQHYYHRDL AARNVLLDNDRLVKIGDFGLAKAVPEGHEYRV REDGDS PVFWYAPECLKEYKFYYASDVWSFGVT LYELLTHCDSSQSPTKFLELIGIAQQGMTVLRLT ELLERGERLPRPDKCPCVYHLMKNCWETEASF RPTFENLIPILKTVHEKYQGQAPSVFVSVC
3533	A	182	3465	FRWLDFFRGSSINSQFEFGRKKENMTSPAKFKKDK EIIAEYDTQVKEIRAQLTEQMKCLDQQCELVRQL LQDLQDFFRKKAEIEMDYSRNLEKLAERFLAKT RSTKDQQFKKDQNVLSPVNCWNLLLNQVKRES RDHTTSLDIYLNNIIPRFVQVSEDSGRLFKKSKEV GQQLQDDLMKVLNELY SVMKTYHMYNADSISA QSKLKEAEKQEEKQIGKSVKQEDRQTPRSPDSTA NVRIEEKHVRSSVKKIEKMKEKRQAKYTENKL KAIKARNEYLLALEATNASVF KYTHDLSDLIDQ CCDLGYHASLNRLRRTFLSAELNLEQSKHEGLD AIENAVENL DATSDKQRLMEMYNNVFCPPMKFE FQPHMGDMASQLCAQPVQSELLQRCLQLQSRL STLKIENEEVKKTMEATLQTIQDIVTVEDFDVSD CFQYSNSMESVKSTVSETFMSKPSIAKRANQQE TEQFYFTKMKEYLEGRNLITKLQAKHDLLOKTL GESQRTDCSLARRSSTVRKQDSSQAIPLVVESCIR FISRHLQHEGIFRVSGSQVEVNDIKNAFERGDP LAGDQNDHDMDSIAGVLKLYFRGLEHPLFPKDF HDLMACVTMDNLQERALHIRKVLLVLPKTTLLI MRYLFAFLNHL SQFSEENMMDPYNLAICFGPSL MSVPEGHDQVSCQAHVNELIKTIIQHENIFPSPRE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LEGPVYSRGGSMEDYCDSPHGETTSVEDSTQDV TAEHHTSDDECEPIEAIKFDYVGRtarelsfkk GASLLLYQRASDDWWEGRHNGIDGLIPHQYIVV QDTEGTVVERSSPKSEIEVISEPPEEKVTARAGAS CPSGGHVADIYLANINKQRKRPESGSIRKTFRSDS HGLSSSLTDSSSPGVGASCRPSSQPMSQSLPKEG PDKCSISGHGSLNSISRHSSSLKNRLDSPQIRKTAT AGRSKSFNHRPMDPEVIAQDIEATMNSALNELR ELERQSSVKHTPDVVLDLTLEPLKTSPVVAPTSEPS SPLHTQLLKDPEPAFQRSASTAGDIACAFRPVKS VKMAAPVKPPATRPKPTVFPKTNATSPGVNSST SPQSTDKSCTV
3534	A	1	2640	FRRFVCPASRRPAAGLRDAASSAPRGMASEGPRE PESEGIKLSADV KPFVPRFAGLNVA WLESSEACV FPSSAATYYPFVQEPPTVEQKIYTEDMAFGASTFP PQYLSSEITLHPYAYSPYTLSTQNVYSVPGSQY LYNQPSCYRGFQTVKHNENTCPLPQEMKALFK KKTYDEKKTQYDQKFDSEADGTISSEIKSARG HHLSIYAENSLKSDGYHKRTDRKSRIIAKNVST KPEFEFTLDFPELQGAENNMSEIQKQPKWGPVH SVSTDISLLREVVKPAAVLKGEIVVKNNPNESV TANAATNSPSCRELSWTPMGYVVRQTLSTELS AAPKNVTSMINLKTIASSADPKNVSPSSEALSSD PSYNKEKHIIHPTQKSKASQGSLEQNEASRKNK KKKEKSTSKYEVLTVQEPPIEDAEFFPNLAVAS ERRDRIETPKFQSKQQPDNFKNNVKKSQLPVQL DLGGM LTALEKKQHSQHAKQSSKPVVSVGAV PVLKKECASGERGRRMSQMKTPHNPLDSSAPLM KKGKQREIPKAKKPTSLKKILKERQERKQRLQE NAVSPAFTSDDTDQGESGGDDQFPEQAELSGPEG MDELISTPSVEDKSEPPGTTELQDTEASHLAPN HTTFPKIHSRRFRDYCSQMLSKEVDACVTDLLKE LVRFQDRMYQKDPVKA KTKRRLVLGLREV LKH LKLKLLKCVIISPNC EKIQSKGGLDDTLHTIDYA CEQNIPFVFALNRKALGRSLNKA VPVSVVGIFS YDGAQDQFHKMVELTVAARQAYKTMLENVQOE LVGEP\SLRHLPA YPHRAPAALQKMAPQPVKEK EEPHYIEIWKKHLEAYSGCTLELESLEASTSQM MNLNL
3535	A	1747	983	LFQFQVCRSVLSPRAAGCTWSLAPRSRGAAGSPR RYRGPQPQAPPSALPNSRPSVAGREMVVLSV PAEVTVILLDIEGTTPIAFVKDILFPYIEENVKEY LQTHWEEECQQDVSLLRKQVFADVPAVRKW REAGMKVYIYSSGSVEAQKLLFGHSTEGDILELV DGHFDTKIGHKVESESYRKIADSIGCSTNNILFLT DVTREASAAEEADVHVAVVVRPGNAGLTDEK TYYSLITSFSELYLPSST
3536	A	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTS IESRGRPAASAGLRRDRCALRRWPLRRAPLARAT RRRAGSPRRCAPRPRACPGWSRARHQPGGLCL LLLLLCQFMEDRSAQAGNCWLRQA KNGRCQVL YKTELSKEECSTGRLSTSWTEEDVNDNTLFKW MIFNGGAPNCIPCKETCENVDCGPGKKCRMNKK NKPRCVCAPDCSNITWKGPVCGLDGKTYRNECA LLKARCKEQPELEVQYQGRCKKTCRDVFCPGSS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TCVVDQTNNA YCVTCNRJCPEPASSEQYL CGND GVTYSASACHLRKATCLLGRSIGLAYEGKCIKAK SCEDIQCTGGKKCLWDFKVGRGRCSLDELCPD SKSDEPVCASDNATYASECAMKEAACSSGVLL VKHSGSCNSISEDTEEEEEDEDDQYSFPISILEW
3537	A	285	2123	IGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRF LTSIPTGIPEDATTLYLQNNQINNAGIPSDLKNLL KVERIYLYHNSLDEFPTNLPKYVKELHLQENNIR TITYDSLSKIPYLEELHLDNNSVSAVSIEGAFRD SNYLRLFLSRNHLSTIPWGLPRTIEELRLDDNRIS TISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFF NLVNLTELSLRNSLTAAPVNLPGTNLRKLYLQ DNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQ GIFDDLNDITQLILRNPWYCGCKMKWVRDWL QSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELF DCKDSGIVSTIQITTAIPNTVYPAQGWPAVTK QPDIKNPKLTKDHQTTGSPSRKTITITVKSVTSDTI HISWKLALPMTALRLSWLKLGHSPAFGSITETIVT GERSEYLVTALEPDSYKVCVMVPMETSNLYLFD ETPVCIETETAPLRMYNPTTTLNREKEKEPKYKNP NLPLAAIIGGAVALVTIALLALVCWYVHRNGSLF SRNCAYSKGRRRKDDYAEAGTKKDNSILEIRETS FQMLPISNEPISKEEFVIHTIFPPNGMNLKNNH
3538	A	877	6184	WNVKPSLLVVQLFKFSDKEEHEQNDSSISGKTGET GVEEMIA TRKVEQDSKETVKLSHEDDHILEDAGS SDISSDAACTNPNTENSLVGLPSCVDEVTECNL ELKDTMGIADKTENTLERNKIEPLGYCEDAESNR QLESTEFNKSNEVVDTSTFGPESNILENAICDVP DQNSKQLNAIESTKIESHETANLQDDRNSQSSSV SYLESKSVKSKHTKPVHSKQNMTTDAPKIVAA KYEVIHSKTKVNVKSVKRNTDVPESQQNFHRPV KVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKK TLQDQTLVQIFKPLTHSLSDKSHAHPGCLKEPHH PAQTGHVSHSSQKQCHKPQQQAPAMKTN SHVK EELHPGVEHFKEEDKLKLKPEKNLQPRQRRSS KSFLDEPPLFIPDNIA TIRREGSDHSSSFESKYMW TPSKQCGFCKKPHGNRFMVGCGRCDWFGDC VGLSLSQAQMG EEDKEYVCVKCAEEDKKTEI LDPDTLENQATVEFHSGDKTMECEKLGLSKHTT NDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKE STTVTCTGEKASKPGTHEKQEMKKKKVVEKGV NVHPAASASKPSADQIRQSVRHSKLDILMKRLTD SNLKVPEEKA AKVATKIEKELFSFRD TDAKYKN KYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIR MSPEELASKELAAWRRREN RHTIEMIEKEQREVE RRPITKITHKGEIEIESDAPMKEQEAAMEIQEPAA NKSLEKPEGSEK/RKEEVDSMSKDTTSQHROHLF DLNCKICIGRMAPPVDDLSPKKVKVVVG VARKH SDNEAESIADALSSTS NILASEFFEEEEKQESPKSTF SPAPRPEMPGTVEVESTFLARLNFIWKGFINMPS VAKFVTKAYPVSGSPEYLTEDLPDSIQVGGRI SPQ TVWDYVEKIKASGTKEICVVRFTPVTEEDQISYT LLFAYFSSRKRYGVAANNMKQVKDMYLIPLGAT DKIPHPLVPFDGPGLELHRPNLLLGLIIRQKLKRQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				HSACASTSHIAETPESAPPIALPPDKKSKIEVSTEE APEEENDFFNSFTTVLHKQRNKPQQNLQEDLPTA VEPLMEVTKQEPKPLRFLPGVLIGWENQPTTLE LANKPLPVDDILQSLGTTGQVYDQAAQSVMQ NTVKEIPFLNEQTNKIEKTDNVEVTDGENKEIK VKVDNISESTDKSAEETS VVGSSSISAGSLTSLSL RGKPPDVSTEAFLTNLSIQSKQETVESKEKTLKR QLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGN VSCSENLVANTARSPQFINLKRDPQAAGRSQPV TTSESKDGDSCRNGEKHMLPGLSHNKEHLTEQIN VEEKLCSAEKNSCVQQSDNLKVAQNPSVENIQT SQAQAKPLQEDILMQNIETVHPFRGSAVATSH FEVGNTPSEFPKSTFTSRSTSPRTSTNFSMPMRP QQPNLQHLKSSPPGFPFPFPNFPQSMFGFPPHL PPPLPPPGFGFA\QNPMVPWPPVV\HLPQGPQR MMGPLSQASRYIGPNFYQVKDIRRPERRHSDP WGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKR ERHEKEWEQESERHRRDRSQDKDRDRKSREEG HKDKERARLSHGDRTDGKASRDSRNVDKKPD KPKSEDEKDKEREKSKHREGEKDRDRYHKDR DHTDRTKSKR
3539	A	157	1769	GSWTVELSLKPSASPSLKWVCLPGAAA\NKHRS GAGGLIRSLIQCTWAPAGPARRGGRIEDFPYLF FQLTHCQQRICSVTQAGVQWCDHSSLQPQTGL NQSSHL SLLSSRDYRMLSSFNEFWQDRFWLPP NVTWTELEDRDGRVYPHPQDLLAALPLALVLLA MRLAFERFIGLPLSRWLGVDRQTRRQVKPNATL EKHFLTEGHRPKPQLSLLAAQCGLTLQQTQRW FRRRRNQDRPQLTKKFCEASWRFLFYLSFFVGG SVLYHESWLWAPVMCWDRYPNQLTLSCPAADS EA\SLYWWYLLELGFYLSLLIRLPFDVKRKG SSIKPRPHYDPPSTA\DFKEQVIHFFVA VILMTFSY SANLLRIGSLVLLLHDSSDYLLACKMVNYMQY QQVCDALFLIFSFFVYTRLVLFPTQILYTTYESI SNRGPFPGYFFNGLMLLQLLHVFWSCLILRML YSFMKKGQMEKDIRSDVEESDSSEEAAAAQEPL QLKNGTAGGPRPAPTDGPRSRVAGRLTNRHTTA T
3540	A	267	1397	SPAGYCHSGLLPGCSRSA/CADLAKHQELPGKKL LSEKKLKRYFVDYRRVLVCGNGGAGASCFHSE PRKEFGGPDGGDGGNGGHVILRVDQQVKSLSV LSRYQGFGSGEDGSKNCFGRSGA VLYIRVPVGT VKEGGRVADLSCVGDEYIAALGGAGGKGNRF FLANNRPAVPTCTPGQPQQRVLHLELKTVAHA GMVGFPNAGKSSLLRAISNARPAVASYPFTLKP HVGIVHYEHLQIAVADIPGIIRGAHQNRGLGSA FLRHIERCRLLFVVDLSQPEPWTQVDDLKYELE MYEKGLSARPHAIVANKIDLPEAQANLSQLRDH LGQEVIVLSALTGENLEQLLLHLKVLYDAYAEA ELGQGRQPLRW
3541	A	1	8008	DTQVSETLKRFAKVTTASVKERREILSELGKCV AGKDLPEGAVKGLCKLFCFLTHRYRDAASRRAL QAAIQQLAEAQPEATAKNLLHSLQSSGIGSKAGV PSKSSGSAALLALTWTCLLVRIVFPSRAKRQGD WNKLVEVQCLLLLEVLGSGSHKHAVDGAVKKLT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KLWKENPGLVEQYLSAILSLEPNQNYAGMLGLL VQFCTSHKEMDVVSQHKSAALLDFYMKNILMSK VKPPKYLLDSCAPLLRYLSHSEFKDILPTIQKSL LRSPENVETISSLLASVTLDLSQYAMDIVKGLAG HLKSNSPRLMDEAVLALRNLARQCDSSAMESL TKHLFAILGGSEGKLTVVAQKMSVLSGIGSVSHH VVSGPSSQVLNGIVAELFIPFLQEVHEGTLVHA VSVLALWCNRFTMEVPKKLTEWFKKAFSLKTST SAVRHAYLQCMLASYRGDTLLQALDLLPLLIQT VEKAASQSTQVPTITEGVAAALLLKL SVADSQA EAKLSSFQWLIVDEKKQVFTSEKFLVMASEDAL CTVLHLTERLFLDHPHRLTGNKVQQYHRAVLA VLLSRTWHVRRQAQQTVRKLLSSLGGFKLAHGL LEELKTVLSSHKVLPLEALVTDAGEVTEAGKAY VPPRVLQEALCVISGVPGLKGDVTDTEQLAQEM LIISHHPSLVAVQSGLWPALLARMKIDPEAFITRH LDQIIPRMTTQSPLNQSSMNAMGSLSVLSPDRVL PQLISTITASVQNPALRLVTREEFAIMQTPAGELY DKSIIQSAQQDSIKKANMKRENKAYSFKEQIIELE LKEEIKKKKGIKEEVQLTSKQKEMLQAQLDREA QVRRRLQELDGELEAALGLLDIILAKNPGLTQYI PVLVDSFLPLLKSPLAAPRIKNPFLSLAACVMPSR LKALGTLVSHVTLRLLKPECVLDKSWCQEELSV AVKRAVMLLHTHTITSRVGKGEPGAAPLSAPAFS LVFPFLKMVLTEMPHHSEEEEEWMAQILQILTVQ AQLRASNTPPGRVDENGPELLPRVAMLRLLTW VIGTGSPRLQVLASDTLTTLCASSGDDGCAFAE QEEVDVLLCALQSPCASVRETVLRGLMELHMVL PAPDTDEKNGLNLLRRLWVVKFDKEEIRKLAEL RLWSMMGLDLQPDLCSLLDIVYHEAAVRQAG AEALSQAVARYQRQAAEVMGRLEIYQEKLYR PPPVLDALGRVISESPDQWEARCGALALANKLS QYLDSSQVKPLFFQFPDALNDRHPDVRKCMULD AALATLNTHGKENVNSLLPVFEEFLKNAPNDAS YDAVRQSVVVLMSGSLAKHLKSDPKVKPIVAKL IAALSTPSQQVQESVASCLPPLVPAIKEDAGGMIQ RLMQQLESDDKYAERKGAAYGLAGLVKGLGILS LKQQEMMAALTDAIQDKKNFRREGALFAFEM LCTMLGKLFEPYVVHVLPHELLCFGDGNQYVRE AADDCAKAVMSNLSAHGVKLVLPSELLAALEES WRTKAGSVELLGAMAYCAPKQLSSCLPNIVPKL TEVLTDSHVKVQKAGQALRQIGSVIRNPEILAI APVLLDALTDPSRKTQKCLQTLDTKFVHFIDAP SLALIMPIVQRAFQDRSTDTRKMAAQHGNMYSL TDQKDLAPYLPVTPGLKASLLDPVPEVRTVSAK ALGAMVKMGESCFEDLLPWLMTLTYEQSSV DRSGAAQGLAEVMAGLGVEKLEKLMPEIVATAS KVDIAPHVRDGYIMMFNYLPITFGDKFTPYVGPII PCILKALADENEFVRDTALRAGQRVISMAYETA ALLLPQLEQGLFDDLWRIRFSSVQLLGDLLFHISG VTGKMTTETASEDDNFGTAQSNKAIITAGVERR NRVLAGLYMGRSDTQLVVRQASLHVWKIVVSN TPRTLREILPTLFGLLGFLASTCADKRTIAARTL GDLVRKLGEKILPEIIPILEEGLRSQKSDERQGVCI GLSEIMKSTSRDAVLVYFESLVPTARKALCDPLE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EVREAAAKTFEQLHSTIGHQALEDILPFLKQLD DEEVSEFALDGLKQVMAIKSRVVLVLPYLVPKLTTP PVNTRVLAFLSSVAGDALTRHLGVLPVLMAL KEKLGTPDEQLEMANCQAVILSVEDDTGHRHIE DLLEATRSPEVGMQRQAAAILNIYCSRSKADYTS HLRSLVSGLIRLFNDSSPVVLEESWDALNAITKK LDAGNQLALIEELHKEIRLIGNESKGEHVPGFCLP KKGVTSLPVLREGVLTGSPEQKEEAAKALGLVI RLTSADALRPSVVSITGPLIRILGDRFSWNVKAAL LETLSLLAKVGIALKPFLPQLQTTFTKALQDSNR GVRLKAADALGKLISIHKVDPLFTELLNGIRAME DPGVRDTMLQALRFVIQGAGAKVDAVIRKNIVS LLLSMLGHDEDNTRISSAGCLGELCAFLTEEELS AVLQQCLLADVSGIDWMVRHGRSLALSVAVNV APGRLCAGRYSSDVQEMILSSATADRIPIA VSGV RGMGFLMRHHIETGGGQLPAKLSSLFVKCLQNP SSDIRLVAEKMIWWANKDPLPLDPQAIKPILKA LLDNTKDKNTVVRAYSDAQIVNLLKMRQGEEVF QSLSKILDVASLEVLNEVNRRLKKLASQADSTE QVDDTILT
3542	A	62	1130	PWNPQDFPGNRGLMG\QKGEIGPPGQQGKKGAP GMP/GLMGNGSPGQPGTPGSKGSGEPGIQGM GASGLKGEPATGSPGEPGYMGLPGIQGKKGDK GNQGEKGIQGGQKGENGRQGIQGGQGGHGA GERGEKGEPPVGAIGSKGESGVDGLMGAPGK GQPGDPGPQGGPGLDGKPGREFSEQFIRQVCTDV IRAQLPVLLQSGRIRNCDHCLSQHSGSPGIPGPPGI GPEGPRGLPGLPGRDGVPLVGVPGRPVGRGLK GLPGRNGEKGSGQGFYGPGEQGGPPGPPGPPGI SKEGPPGDPGLPGKGDHKGKPGIQGQPPGPGICD PSLCFSVIARRDPFRKGPNY
3543	A	654	194	PARSLEKMKASVVL SLLGYLVVPSGAYILGRCTV AKKLHDGGLDYFERYSLENWVCLAYFESKFNP AIYENTREGYTGFGLFQMRGSDWCGDHGRNRC HMSCSALLNPNLEKTIKCAKTIVKGEKMGAWP TWSRYCQYSDTLARWLDGCKL
3544	A	2	1074	SCRLAAGRLAQWLLRASRSGMLRAGWL RGA LALLAARVVA AFEPITVGLAIGAASAITGYLSY NDIYCRFAECCREERPLNASALKLDLEEKLFQGH LATEVIFKALTGFRNNKNPKKPLTSLHGWAGT GKNFVSQMGAEHLHPKGLKSNFVHLFVSTLHFP HEQIKLYQDQLQKWIRGNVSACANSVFIDEM DKL\HPGII\AIKPFLDYEHVERVSYRKAIFILS NAGDLITKTALDFWRAGRKRREDIQLKDLEPVL SVGVFNKHSGLWHSGLIDKNLIDYFIFLPLEYR HVKMCVRAEMRARGSAIDEDIVTRVAEEMTFFP RDEKIYSDKGCKTVQSRDLFH
3545	A	3	273	SAQGRSWGRFYRQKRHPGIIPMIGLICLGMGSA ALYLLRLALRSPDVW*SWDRKNNPEPWNRSPN DQYKFLAVSTDYKKLKKDRPDF
3546	A	23	591	ALSTETRTDMMRLLLVTSLVVLLWEAGAVPA PKVPIKMVQKHPSEQDPEKAWGARVVEPPEK DDQLVVLFPVQKPKLLTTEKPRGQGRGPILPGT KAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQG EERPLWVMPNHQVLLGPEEDQDHIYHPQ*GSR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GHHCPRPVPRPRLGLGPSLPCPS
3547	A	23	591	ALSTETRTPDMRRLLVTSLVVLLWEAGAVPA PKVPIKMQVKHWPSEQDPEKAWGARVVEPEK DDQLVVLFPVQKPKLLTTEEKPRGQGRGPILPGT KAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQG EERPRLVWMPNHQVLLGPEEDQDHIYHPQ*GSR GHHCPRPVPRPRLGLGPSLPCPS
3548	A	3	1641	TWLPSVPAEEVQQPEMAA VLNAERLEVSVDGLT LSPDPEERPGAEGAPLAAATAATLATWIRSRPG RLRG TARSPGRR AAGGAAEEARRLEQRWGFLE ELYGLALRFFKEKDGKAFHPTYEEKLKLVALHK QVLMGPYNPDTCEVGFDFVLGNDRRREWAAL GNMSKEDAMVEFVKLLNRCCHLFSTYVASHKIE KEEQEKRRKEEEERRRRREEERERLQKEEEKRRR EEEEERLRREEEERRRIEEERLRLEQQKQQIMAAL NSQTAVQFQQYAAQQYPGNYEQQQLRQLQEQ HYQQYMQLYQVQLAQQQAALQKQQEVVVAG SSLPTSSKVECNCTQVI*CFNRQAKTHDSSEKE LEPEAAEEALENGPKESLPVIAAPSMWTRPQIKD FKEKIQDADSVITVGRGEVTVRVPTHEEGSYL FWEFATDNYDIGFGVYFEWTDSPNTAVSVHVSE SSDDDEEEENIGCEEKAKKNANKPLLDEIVPVY RRDCHEEVYAGSHQYPGRGVYLLKFDNSYSLW RSKSVYYRVYYTR
3549	A	1837	3593	PAVLVLEPASQSRKQNTASATAQHWSAQIHKE SFLAPVFTKDEQKHRRPYEFEVERDAKARGLEQF SATHGHTPIILNGWHGESAMDLSCSSESGPGATS FPFVSASTPKIGAISLQALGMDLSGILQAGLIHP VTGQIVNGSLRRDDAATRRRRRGRKKHVEGGMD LIFLKEQTLQAGILEVHEDPGQATLSTTHPEGPGP ATSAPEPATAASSQAEKSIPSKSLDWLRQQADY SLEVPFGFANFSDKPKQRRPRCKEPKLDVSSL GEERVPAIPKEPGLRGFLPENKFNHTLAEPILRDT GPRRRGRRRRSELLKAPSIVADSPSGMGPLFMNG LIAGMDLVGLQNMNRNMPGIPLTGLVGFPAGFAT MPTGEEVKSTLSMLPMMLPGMAAVPQMFGVGG LLSPPMATTCTSTAPASLSSTTKSGTAVTEKTAE DKPSSHVDKTDLAEDKPGPGPFSDQSEPAITTS PVAFNPFILPGVSPGLIYPSMFLSPGMGMALPAM QQAHRHSEIVGLESQKRKKKTKGDNPNSHPEPA PSCEREPSGDENCAEPSAPLPAEREHGAQAGEGA LKDSNNDTN
3550	A	287	39	QLNLNKIATSQKHRDFVAESVGEKPVGSLAGIGE VMDKKLEEGCFDKAYVVLGQFLVLKKDEDLF*E WLRDTGGARTGSRE
3551	A	21	3925	GDILLEVLPPGLEFPRGICLRGLRRTMSLDFGSV ALPVQNEDEEYDEEDYEREKELQQLLTDLPHDM LDDDLSSPELQYSDCEDGTGQPHHPEQLEMS WNEQMLPKSQSVNGPSCQGLEPYNKVTKPYQS SAQNGSPAQEITGSDTFEGLQQQFLGANENSAE NMQIIQLQVLNKAKERQLENLIEKLNESERQIRY LNHQLVIKDEKDGLTSLRESQKLFQNGKEREIQ LEAQIKALETQIQALKVNEEQMIKKSRTTEMALE SLKQQLVDLHHSESQRAREQHSIVMGLTKKY EEQVLSLQKNLDATVTALKEQEDICSRLKDHVK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				QLERNQEAIAKLEKTEIINKLTRSLEESQKQCAHLL QSGSVQVEVAQLQFQLQQAQKAHAMSANMNKA LQEELTELKDEISLYESA AKLGIHPSDSEGELNIEL TESYVDLGIKKVNWKKSKVTSIVQEEDPNEELSK DEFILKLKAEVQRLGNSMKRHLVSQQLNDLK DCHKKIEDLHQVKKDEKSIEVETKTDTSEKPKNQ LWPESSTSDVVRDDILLKNEIQVLQQQNQELKE TEGKLRTNQDL CNQMRQMVQDFDHDKQEAV DRCERTYQQHHEAMKTQIRESLLAKHALEKQQL FEAYERTHLQLRSELDKLNKEVTA VQECYLEVC REKDNLELTLRKTTKEQQQTQEKIKEKLIQLEK EWQSKLDQTIKAMKKKTLDCGSQTDQVTTSDVI SKKEMAIMIEEQKCTIQQNLEQEKDIAIKGAMKK LEIELELKHCEINITKQVEIAVQNAHQRWLGELPE LAEYQALVKA EQKWEQHEVSVNKRISFAVSE AKEKWKSELENMRKNILPGKELEEKIHS LQKELE LKNEEVPVIRAE LAKARSEWNKEKQEEIHRIQE QNEQDYRQFLDDHRNKINEVLAAAKEDFMKQK TELLQKETELQTC LDQSRREW TMQEA KRIQLEI YQYEE DILTVLG VLLSDTQKEHISDS EDKQLLEI MSTCSSK WMSVQYFEKLGKCIQKAFQDTLPLL ENADPEWKKRNMAELSKDSASQGTGQDGP AGHHAQPLALQATEAEADKKKVLEIKDLCCGHC FQELEKAKQECQDLKGKLEKCCRHLQHLEKHK AVVEKIGEENNVVEELIEENNDMKNKLEELQT LCKTPRSL SAGAIENACLPCSGGALEELRGQYIK AVKKIKCDMLRYIQESKERAEMVKA EVL*ERQ ETARKMRKY YLCLQ QILQDDGKEGA EKIMNA ASKLATMAK LLETPISSKSQSKTTQSGMSK
3552	A	771	375	ARTROTSGQAREPEKESPAPGGGGLAEIRSQQ SQTSRIPPLAKDQAVEAMFPPARGKELLSFEDVA MYFTREEWGHLNWGQKDLYRDVMLENYRNMV LLVYFQFDAAIPLC* TSLAHSSWLQLYFRLYF
3553	A	76	72	PGVRGVEAPGGVAPGRNAMRRGERRDAGGPRP ESPVPAGRASLEPPDGPSAGQATGPGEGRSTE SEVYDDGTNTFFWRAHTLTVLFILCTLG YVTLL EETPQDTAYNTKRGIVASILVFLCFGVTQAKDGP FSRPHPAYWRFWLCVSVVYELFLIFILFQTVQDG RQFLKYVDPKLG VPLPERDYGGNCLYDPDNET DPFHNIWDKLDGFVPAHFLGWYKTLMIRDWW MCMISVMFEFLEYSLEHQLPNFSECWWDHWIM DVLVCNGLGIYCGMKTLEWLSLKT YKWQGLWN IPTYKGKMKRIAFQFTPYSWVRFEWKPASSLR WLAVCGIILVFLLAELNTFY LKFVLWMPPEHYLV LLRLVFFVNVGGVAMREIYDFMDDPKPHKKLGP QAWLVAAITATELLIVVKYDPHTLTLSLPFYISQC WTLGSLALTWTVWRFFLRDITLRYKETRWQK WQNKDDQGSTVGNGDQHPLGLDEDLLGPGVAE GEGAPTPN*PRGPAPRLPSAPRAVCGASSRR
3554	A	2	2106	FDEFALPSPSLQTSWSFGPMSRRALRRLRGEQR QGEPLGPGALHFDLRDDDDAE EGP KRELGVRR PGGAGKEGVRVNNRFELINIDDEDDPVVNGERS GCALTD AVAPGNKGRGQRGNTESKTDGDDTET VPSEQSHASGKL RKKKKKQKNKKSSTGEASENG LEDIDRILERIEDSTGLNRP GPAPLSSRKHVLYVE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				HRHLNPDTELKRYFGARAILGEQRPRQRQRVYP KCTWLTTPKSTWPRYSKPGLSMRLLESKKGLSFF AFEHSEYQQAQHKFLVAVESMEPNNIVVLLQT SPYHVDLSLLQLSDACRFQEDQEMARDLVERALY SMECAFHPLFSLTSGACRLDYRRPENRSFYALY KQMSFLEKRGCPRTALEYCKLILSLEPDEDPLCM LLLDHLALRARNYEYLIRLFQEWVVGASLAHRN LSQLPNFAFSVPLAYYFLLSQQTDLPCEQSSARQ KASLLIQQALTMFPGVLLPLESCSVRPDASVSSH RFFGPNAEISQPPALSQVLNLYLGRSHFLWKEPA TMSWLEENVHEVLQAVDAGDPAVEACENRRKV LYQRAPRNIHRHVILSEIKEAVAALPPDVTTQSV MGFDPLPPSDTIYSYVRPERLSPISHGNTIALFFRS LLPNYTMGERPEEGVAGGLNRNQGLNRLMLA VRDMMANFHLNDLEAPHEDDA*GEGEWD
3555	A	2	2106	FDEFSALPSPSLQTSWSFGPMSRRALRRLRGEQR GQEPLGPGALHFDLRDDDDAEEEGPKRELGVRR PGGAGKEGVRVNNRFELINIDDEDDPVVNGERS GCALTDVAVPGNKGRGQRGNTESTKTDGDDTET VPSEQSHASGKLRRKKKKKQKNKKSSTGEASENG LEDIDRILERIEDSTGLNRPGAPLSSRKHVLYVE HRHLNPDTELKRYFGARAILGEQRPRQRQRVYP KCTWLTTPKSTWPRYSKPGLSMRLLESKKGLSFF AFEHSEYQQAQHKFLVAVESMEPNNIVVLLQT SPYHVDLSLLQLSDACRFQEDQEMARDLVERALY SMECAFHPLFSLTSGACRLDYRRPENRSFYALY KQMSFLEKRGCPRTALEYCKLILSLEPDEDPLCM LLLDHLALRARNYEYLIRLFQEWVVGASLAHRN LSQLPNFAFSVPLAYYFLLSQQTDLPCEQSSARQ KASLLIQQALTMFPGVLLPLESCSVRPDASVSSH RFFGPNAEISQPPALSQVLNLYLGRSHFLWKEPA TMSWLEENVHEVLQAVDAGDPAVEACENRRKV LYQRAPRNIHRHVILSEIKEAVAALPPDVTTQSV MGFDPLPPSDTIYSYVRPERLSPISHGNTIALFFRS LLPNYTMGERPEEGVAGGLNRNQGLNRLMLA VRDMMANFHLNDLEAPHEDDA*GEGEWD
3556	A	3388	1650	KTRGTMFYYPNVLQRHTGCFATIWLAAATRGSR VKREYLRVNVVKTCEEILNYVLVRVQPPQGLP RPRFSLYLSAQLQIGVIRVYSQQCQYLVEDIQHIL ERLHRAQLQIRIDMETELPSLLLPNHLAMMETLE DAPDPFFGMMSVDPRLPSPFDIPQIRHLLAAIPE RVEEIPPEVPTPEPERIPVTVLPPEAITILEAEPIR MLEIEGERELPEVSRRELDLLIAEEEEAILLEIPRL PPPAPAE*GOELLDQVGCQCWEGSPHFSCPFPLR VEGMGEALGPEELRLTGWEPGALLMEVTPPEEL RLPAPPSPERRPPVPPPPRRRRRRLLFWDKETQI SPEKFQEQQLQTRAHCWECPMVQPPERTIRGPAEL FRTPTLSGWLPELLGLWTHCAQPPPKALRREL EEAAAEERKIEVPSEIEVPREALEPSVPLMVSL EISLEAAEEKSRISLIPPEERWAWPEVEAPEAPA LPVVPELPEVPMEMPLVLPPELELLSLEAVHRAV ALELQANREPDFSSLVSPLSPRRMAARVFYLLLV LSAQQLHVQKEKPYGRLLIQGPRFH
3557	A	3388	1650	KTRGTMFYYPNVLQRHTGCFATIWLAAATRGSR VKREYLRVNVVKTCEEILNYVLVRVQPPQGLP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RPRFSLYLSAQLQIGVIRVYSQQCQYLVEDIQHIL ERLHRAQLQIRIDMETELPSLLLPNHLAMMETLE DAPDPFFGMMSVDPRLPSPFDIPQIRHLLAEAAIPE RVEEIPPEVPTPEPREPERIPVTVLPPEAITLEAEPIR MLEIEGERELPEVSRRELDLLIAEEEEAILLEIPRL PPPAPAE*GQELLDQVGCQCWEGSPHFSCFFPLR VEGMGEALGPEELRLTGWEPGALLMEVTPPEEL RLPAPSPERRPPVPPPPRRRRRRLLFWDKETQI SPEKFQEQQLQTRAHCWECPMVQPPERTIRGPAEL FRTPTLSGWLPEELLGLWTHCAQPPPKALRREL EEAAAAEEERRKIEVPSEIEVPREALEPSVPLMVSL EISLEAAEEEEKSRLIPPEERWAWPEVEAPEAPA LPVVPELPEVPMEMPLVLPELELLSLEAVHRAV ALELQANREPDFSSLVSPSPRRMAARVFYLLLV LSAQQILHVQKEKPYGRLLIQGPRFH
3558	A	489	2360	IRPRPRGRRRALDSPNAAAPPVYVCRSPGEPTSL VNMASEDIAKLAETLAKTQVAGGQLSFKGKSLK LNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEA ARVIAKAL*KKSELKRCHWSDMFTGRLRTEIPPA LISLGEGLITAGACLVELDLSDNAFGPDGVQGF ALLKSSACFTLQELKLNNCGMGIGGGKILAAALT ECHRKSSAQGKPLALKVFVAGRNRLENDGATAL AEAFRVIGTLEEVMHPQNGINHPGITALAQAFV NPLLRVINLNDNTFTEKGAVAMAETLKTTLRQVE VINFGDCLVRSGGAVAIADAIRGGLPKLKELNLS FCEIKRDAALAVAEAMADKAELEKLDLNGNTLG EEGCEQLQEVLEGFNMAKVLASLSDDDEDEEEEE EGEEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQRG QGEKSATPSRKILDNPNTGEPAPVLSSPPADVSTF LAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVS AFLKVSSVFKDEATVRMAVQDAVDALMQKAFNS SSFNSNTFLTRLLVHMGLLKSEDKVKAIANLYGP LMALNHMVQQDYFPKALAPLLLAFTVKPNSALE SCSFARHSLQLTYKV
3559	A	489	2360	IRPRPRGRRRALDSPNAAAPPVYVCRSPGEPTSL VNMASEDIAKLAETLAKTQVAGGQLSFKGKSLK LNTAEDAKDVIKEIEDFDSLEALRLEGNTVGVEA ARVIAKAL*KKSELKRCHWSDMFTGRLRTEIPPA LISLGEGLITAGACLVELDLSDNAFGPDGVQGF ALLKSSACFTLQELKLNNCGMGIGGGKILAAALT ECHRKSSAQGKPLALKVFVAGRNRLENDGATAL AEAFRVIGTLEEVMHPQNGINHPGITALAQAFV NPLLRVINLNDNTFTEKGAVAMAETLKTTLRQVE VINFGDCLVRSGGAVAIADAIRGGLPKLKELNLS FCEIKRDAALAVAEAMADKAELEKLDLNGNTLG EEGCEQLQEVLEGFNMAKVLASLSDDDEDEEEEE EGEEEEEEAEEEEEEDEEEEEEEEEEEEEEPQQRG QGEKSATPSRKILDNPNTGEPAPVLSSPPADVSTF LAFPSPEKLLRLGPKSSVLIAQQTDTSDPEKVVS AFLKVSSVFKDEATVRMAVQDAVDALMQKAFNS SSFNSNTFLTRLLVHMGLLKSEDKVKAIANLYGP LMALNHMVQQDYFPKALAPLLLAFTVKPNSALE SCSFARHSLQLTYKV
3560	A	2	1198	FVRELPRPRGAATAAIMVSVINTVDTSHEDMIH DAQMDYYGTRLATCSSDRSVKIFDVRNGGQILIA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DLRGHEGPVWQVAWAHPMYGNILASCSYDRKV IIVREENGTWEKSHEHAGHDSSVNSVCWAPHDY GLILACGSSDGAISLLTYTGEGQWEVKINNAHT IGCNAVSWAPAVVPGSLIDHPSGQKPNYIKRFAS GGCDNLIKLVKEEEDGQWKKEQKLEAHSWVR DVAWAPSIGLPTSTIASCSQDGRVFIWTCDDASS NTWSPKLLHKFNDVVWHVWSITANILAVSGGD NKVTLWKESVDGQWVCISDVNKGQGSVSASVT EGQQNEQ*QDRWGLAPHPAPGLPLPGPTNQTT GKSPQLQQDYFPRRSYRCSHRLIICLVIGDAL
3561	A	540	86	WRVKEMTSTLPKALGRKTASRSHITLQGGSCCP VLWTAKLRCKLRFPLPPPPSSSAWPWQGWGI RGEQEAEGPLGETGPPVGPGLSGLRQWRKLIKGR YGEWRGSGQKTGQPS*TTMQGGETEENRTETTT GNKQRESEAPWVRHTYIT
3562	A	1920	242	PMMAMPFFERFKSSIQRPSVLVLSQNTKRESGR KVQSGNINAAKTIADIIRTCLGPKSMMKMLLDP MGGIVMTNDGNAILREIQVQHPAAKSMIEISRTQ DEEVGDGTTSVIILAGEMLSVAEHFLEQQMHPTV VISA YRKALDDMISTLKKISIPVDISDSMMMLNIN SSITTKAISRWSSLACNIALDAVKMVQFEENGRK EIDIKKYARVEKIPGGIIEDSCVLRGVMINKDVTH PRMRRYIKNPRIVLLDSSLEYKKGESQTDIEITRE EDFTRILQMEEEYIQQLCEDIIQLKPDVVITEKGIS DLAQHYLMRANITAIRVRKTDNNRIARACGARI VSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDC KDPKACTILLRGASKEILSEVERNFDAMQVCRN VLLDPQLVPGGGASEMAVAHALTEKSKAMTGV EQWPYRAVAQALEVIPRTLQNCGASTIRLLTSLR AKHTQENCETWGVNGETGTLVDMKELGIWEPL AVKLQTYKTA VETAVLLLRIDDIVSGHKKKGDD QSRQGGAPDAGQE
3563	A	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAV DDLQFEFGNAATSLTANPDATTVNIEDPGETPK HQPGSPRGSGREEDDELLGNDSDSKTELLAGQK KSSPFWTFEYYQTFDVTYQVFDRIKGSLLPIG KNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLS NFLIHLGEKTYHYVPEFRKVSIAATIIYAYAWLVP LALWGFLMWRNSKVMNIVSYSFLEIVCVYGYSL FIYIPTAILWIIPHKAVRWILVMIALGISGSLLAMT FWPAVREDNRRVALATIVTIVLLHMLLSVGCLA YFFDAPEMDHLPTTTATPNQTVAAAKSS
3564	A	1	328	NSRVDDFVAHLQRPLLGPASCLGILRPAMTAHSF ALPGIIFTTFWGLVGIAGPWFVPKGPNRGVIIITML VATAVCCYLFWLIALAQLNPLFGPQLKNETIWW VRFLWE
3565	A	2	1081	FVTDFFPARSMAATSLMSALAAARLLQPAHSCSLRL RPFHLAAVRNEAVVISGRKLAQKIQEVRQVEE WVASGNKRPHLSVILVGENPASHSYVLNKTRAA AVVGINSETIMKPASISEEELNLNKLNNDDNVD GLLVQLPLPEHIDERRICNAVSPDKDVGDFHVIN VGRMCLDQYSMLPATPWGVWEIKRTGIPTLGK NVVVAGRSKNVGMPIAMLLHTDGAHERPGGDA TVTISHRYTPKEQLKKHTILADIVISAA GIPNLITA DMIKEGAAVIDVGINRVHDPVTAKPKLVGDVDF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EGVRQKAGYITPVPGGVGPMTVAMLMKNTIIAA KKVLRLEEREVLKSKELGVATN
3566	A	3	1130	SCRRGRQQRRNVSLSSQFAHTMAAPAQQTTPQ GGGKRKGKAQYVLAKRARRCDAGGPRQLEPGL QGILITCNMNERKCV EEA YSLLNEYGDDMYGPE KFTDKDQQPSGSEGEDDDAEALKEVGDIKAS TEMLRRFQSVESGANNVVFIRTLGIEPEKLVHHI LQDMYKTKKKKTRVILRMLPISGTCKAFLEDMA KYAETFLEPWFKAPNKGTFQIVYKSRNNSHVNR EEVIRELAGIVCTLNSENKVDLTNPQYTVVVEIHK AVCCLSVVKDYMLFRKYNLQEVVKSPKDPSQLN SKQNGKEAKLESADKSDQNNTAEGKNNQQVP ENTEELGQTKPTSPNPQVVNEGGAKPELASQATE GSKSNENDFS
3567	A	248	3498	GKKDSSPWTCPFHPPLQLFFVIRNTRQLGDFHLA KIKVRNYWTADGDLDIGAKNVKLYVNRNLIFNG KLDKGDREAPADHSILVDQKNEKSEQLEEAMNA HSEESKGTHEMAGASGDKELGLGCSPPAETLAD AKLSSQGNVSGKRKNSTNCRKDSLSQLEEYLRLS AVPTSMGDMPSAPATSPPVKCPPVHEEPSLIQQL ENLMGRKICEPPGKTPSWLQPSPTGKDRKQGGGR KPKPLWLSPEKPLAWKGRLPDSDVIGEGPGETEA RDKGLRHEPGWGTSRSVNTKERPQRATTKVHSD DSDIFNQPPNRERPASGRRGSRKDAGSSSHGDDQ PASREDTWSSRTPSRSRWRSEQHTLHESWSSL AFDRSHRGRISNTELPDILDELQKSSRHSDDL PSKKGEQPGLSRGQDGYSGETDAGGDFKIPVLPY GQRLVIDIKSTWGDRIYVGLNGIEIFSSKGEVQI SNIKADPPDINILPAYGKDPVVNTLIDGVNRTQ DDMHVWLAPFTRGRSHSITIDFTHPCHVALIRIW NYNKSRIHSFRGVKDITMLLDTCIFEGEIAKASG TLAGAPEHFGDITLFTDDDI EAIFYSDMFLLD VGSLDSLQDEEAMRRPSTADGEGDERPFTQAGL GADERIPELELPSSSPVPQVTTPEPGIYHGICLQLN FTASWGDHLHYLGLTGLEVVGKEGQALPIHLHQS ASPRDLNELPEYSDDSRDLKLDGTNITMEDEH MWLIPFSPGLDHVVITIRLDRAESIAGLRFWYNK SPEDTYRGAKIVHVS LDGLCVSPPEGFLIRKGP NCHFDFAEILFVDYLRAQLLPQARRLDMRSL CASMDYEA PLMPCGFIFQFQLLTSWGDPPYYIGLT GLELYDERGEKIPLSENNIAAFPDSVNSLEGVGG DVRTPKLIDQVNDTSDGRHMLAPILPGLVNR VYVIFDLPTTVSMIKLWNYAKTPHRGVKEFGLL VDDL VYNGILAMVSHLVGGILPTCEPTVPYHTI LFTEDRDIRHQEKHTTISNQAEDQDVQMMNENQ IITNAKRKQSVVDPALRPKTCISEKETRRRRRC
3568	A	50	1724	AQGGTLSAASRFCRGGLLPWLHPASEMAATLD LKSKEEKDAELDKRIEALRRKNEALIRRYQIEE DRKKALEGVA VTAPRKGRSVEKENVAVESEKN LGPSRRSPGTPRPPGASKGGRTPPQQGGRAGMG RASRSWEGSPGEQPRGGGAGGRGRRGRGRGSPH LSGAGDTSISDRKSKEWEERRRQNI EKMN EEME KIAEYERNQREGVLEPNPVRNFLDDPRRRSGPLE ESERDRREESRRHGRNWGGPDFERVRCGLEHER QGRRAGLGSAGDMTLSMTGRERSEYLRWKQER

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EKIDQERLQRHRKPTGQWRREWDAEKTDGMFK DGPVPAHEPSHRYDDQAWARPPKPPTFGFELSQ HKAEASSRRRRKSSRPQAKAAPRAYSDHDDRWE TKEGAASPAPETPQPTSPETSPKETPMQPPEIPAP AHRPPEDEGEENE GEEDEE WEDISEDEEEEEIEVE EGDEEPAQDHOAPEAAPTGPCEQAHGVPFSP EEPLLEPQAPGTPSSPSPSGHQPVSDWGEEVEL NSPRTTHLAGALSPGEAWPFESV
3569	A	1	912	MGRVGRAGVQLGRRRTTAAERTGQAAAGGP GRALRGQRPDRLRSGGAADSPAAGRGELYCGVLP RSPWFLSERRRRQMADFDTYDDRAYSSFGGGRGS RGSAGGHGSRSQKELPTEPPYTA YVGNLPFNTV QGDIDAIFKDLIRSIVRLVRDKD TDKFKGFCYVE FDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQ DKGGFGFRKGGPDDRGFRDDFLGGRGGSRPGRD RTGPPMGSFRDGPPLRGSNMDFREPTTEERAQR PRLQLKPRTVATPLNQVANPNSAIFGGARPREEV VQKEQE
3570	A	1	912	MGRVGRAGVQLGRRRTTAAERTGQAAAGGP GRALRGQRPDRLRSGGAADSPAAGRGELYCGVLP RSPWFLSERRRRQMADFDTYDDRAYSSFGGGRGS RGSAGGHGSRSQKELPTEPPYTA YVGNLPFNTV QGDIDAIFKDLIRSIVRLVRDKD TDKFKGFCYVE FDEVDSLKEALTYDGALLGDRSLRVDIAEGRKQ DKGGFGFRKGGPDDRGFRDDFLGGRGGSRPGRD RTGPPMGSFRDGPPLRGSNMDFREPTTEERAQR PRLQLKPRTVATPLNQVANPNSAIFGGARPREEV VQKEQE
3571	A	28	131	RHFFGNLCAMRAKWRKKRMRLKRKRMRQ RSK
3572	A	3	1202	QSEPHRKVRVDPVDRPPPHPPPLLVQRALPGQ GQAEAGSDGADAKRRAMAHQTGIHATEELKEFF AKARAGSVRLIKV VIEDEQLVLGASQEPVGRWD QDYDRAVLPLLDAAQPCYLLYRLDSQNAQGFE WLFLAWSPDNSPVRLKMLYAATRATVKKEFGG GHIKDELFGTVKDDLSFAGYQKHLSSCAAPPLT SAERELQQRINEVKTEISVESKHQTLQGLAFPLQ PEAQRALQQLKQKMVNVIQMKLDLERETIELVH TEPTDVAQLPSRVPRDAARYHFFLYKHTHEGDP LESVVFYISMPGYKCSIKERMLYSSCKSRLLDSV EQDFHLEIAKKIEIGDGAELTAEFLYDEVHPKQH AFKQAFAPKPGPGGKRGHKRLIRGPGENGDD
3573	A	49	1869	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEV EEISLLQPQVEESVLNLGKFHSIVRLVAFCPFASS QVALENANA VSEGVVHEDLRLLLETHLP SKKKK VLLGVGDPKIGAAIQEELGYNCQTGGVIAEILRG VRLHFHNLVKGLTDL SACKAQLGLGHSYSRAKV KFNVNVRVDNMIIQSISLLDQLDKDINTFSMRVRE WYGYHFPELVKINDNATYCRLAQFIGNRRELNE DKLEKLEELTMDGAKAKAILDASRSSMGMDISAI DLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAP SLSALIGEAVGARLIAHAGSLTNLAKYPASTVQIL GAEKALFRALKTRGNTPKYGLIFHSTFIGRAAAK NKGRISRYLANKCSIASRIDCFSEVPTSVFGEKLR EQVEERLSFYETGEIPRKNLDVMKEAMVQAEAE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EAAAEITRKLEKQEKKRLKKEKKRLAALALASS ENSSSTPEECEETSEKPKKKKKQKQPEVPQENGM EDPSISFSKPKKKKSFSKEELMSSDLEETAGSTSIP KRKKS TPKEETVNDPEEAGHRSRSKKKRKFSKEE PVSSGPPEAVGKSSSKKKKFKHAKSQED
3574	A	284	2032	CGNERTARLWVQPVVSTMPQASEHRLGRTREPP VNIQPRVGSKLPAFAPRARSKERRNPASGPNMLR PLPPRPGLPDERLKKLELGRGRTSGPRPRGPLRA DHGVPLPGSPPTVALPLSRTNLARSKSVSSGDL RPMGIALGGHRTGELGAALSRLALRPEPPTLRR STSLRRLGGFPPTLFSIRTEPPASHGSFHMISAR SSEPFYSDDKMAHHTLLGSGHVGLRNLGNTCF LNAVQLCLSSSTRPLRDFCLRRDFRQEVPGGGRA QELTEAFADVIGALWHPDSCEAVNPTRFRAVFQ KYVPSFSGYSQQDAQEFLKLLMERLHLEINRRGR RAPPILANGVPVSPRRGGALLEEPELSDDDRANL MWKRYLEREDSKIVDLFGQLKSKLCQACGY RSTTFEVFCDLSLPIPKKGFAGGKVSLRDCFNFLT KEEELESENAPVCDRCRQKTRSTKKLTVQRFPI LVLHLNRFASASRGSIKKSSVGVDPLQRLSLGDF ASDKAGSPVYQLYALCNHSGSVHYGHYTALCR CQTGWHVYNDSRVSPVSENQVASSEGYVLFYQL MQEPPRCL
3575	A	1	2408	RELDLADLPERIKPPYANGLSTSHLRSSSVEDVK LIISEGRPTIEVRRCMPSVICEHTKQFQTISEESN QGSLLTVPGDTSPSPKPEVFSNVPERDLSNVSNH SSFATSPGTASNSKYVSADRNLKNTAPVNTVMD SPVHLEPSSQGVQNKSWEMPVDRLETSTRDF ICPNSNIPDQESSLQSFCSSENKVLKENADFLSLR QTELPGNSCAQDPAFMPQQPCSFPSQSLSDAES ISKHMSLSYVANQEPGILQQKNAVQIISALD TD NESTKDTENTFVLGDVQKTD AFVPVYSDSTIQEA SPNFEKAYTLPVLPSEKDFNGSDASTQLNTHYAF SKLTYKSSSGHEVENSTTD TQVISHEKENKLESL VLTHLSRCDSDLCENAGMPKGNLNEQDPKHC PESEKCLLSIEDEESQQSILSSLENHSQQSTQPEM HKYGQLVKVELEENAEDDKTENQIPQRMTRNK ANTMANQSKQILASCTLLSEKDSSESSPRGRIRLT EDDDPQIHHPKRKRKVS RVPQVQVSPSLLQAKEK TQQSLAAIVDSLKLDEIQPYSSERANPYFEYLHIR KKIEEKRLKLLCSVIPQAPQYYDEYVTFNGSYLLD GNPLSKICIPTITPPPSLSDPLKELFRQQEVVRMKL RLQHSIEREKLIVSNEQEVLRVHYRAARTLANQT LPFSACTVLLDAEVYNVPLDSQSDSKTSVRDRF NARQFMSWLQDVDDKFDKLTCLLMRQQHEA AALNAVQRLEWQLKLQELDPATYKSISIYEIQEF YVPLVDVNDDFELTPI
3576	A	5	1421	LRLAWHDGARWPLGTPRAAAATRREAAALPPVT LALLCLDGVFLSSAENDFVHRIQEELDRFLQKQ LSKVLLFPPLSSRLRYLIHRTAENFDLLSSFSVGE GWRRTVICHQDIRVPSSDGLSGPCRAPASCP SR YHGPRPISNQAAA VPRGARAGR WYRGRKPDQ PLYVPRVLRREQEEWGLTSTSVLKREAPAGRDPEE PGDVGAGDPNSDQGLPVLMTQGTEDLKGPGR CENEPLDPVGPEPLGPESQSGKGMVEMATRF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GSTLQLDLEKGKESLLEKRLVAEEEEDEEEVEED GPSSCEDDYSELLQEITDNLTKKEIQIEKIHLDT SFMEELPGEKDLAHVVEIYDFEPALKTEDLLATF SEFQEGGFRIQWVDDTHALGIFPCRASAAEALTR EFSVLKIRPLTQGTKQSKLKALQRPKLLRLVKER PQTNATVARRLVARALGLQHKKKERPAVRGPLP P
3577	A	102	1998	DTRTPGSLEMGPLQFRDVAIEFSLEEWHCCLDTAQ RNLYRNVMLNYSNLVFLGIVVSKPDLIAHLEQG KKPLTMKRHEMVANPSGPVICSHFAQDLWPEQN IKDSFQKVILRRYEKRGHGNLQLIKRCESVDECK VHTGGYNGLNQCSTTTQSKVFQCDKYGKVFHK FSNSNRHNRHTEKKPFKCIECGKAFNQFSTLITH KKIHTGEKPYICEECGKAFKYSSALNTHKRIHTG EKPYKCDKCDKAFIASSTLSKHEIHTGKKPYKCE ECGKAFNQSSSTLTKHKKIHTGEKPYKCEECGKAF NQSSSTLTKHKKIHTGEKPYVCEECGKAFKYSRIL TTHKRIHTGEKPYKCNKCGKAFIASSTLSRHEFIH MGKKHYKCEECGKAFIWSSVLTRHKRVHTGEKP YKCEECGKAFKYSSTLSSHRSHTGEKPYKCEEC GKAFVASSTLSKHEIHTGKKPYKCEECGKAFNQSS SSSTLTKHKKIHTGEKPYKCEECGKAFNQSSSTLTK HKKIHTGEKPYKCEECGKAFNQSSSTLIKHKKIHT REKPYKCEECGKAFHLSTHLTTHKILHTGEKPYR CRECGKAFNHSATLSSHKKIHSGEKPYECDKCG KAFISPPSSLSRHEIHTGEKP
3578	A	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPLRP LSRHPLSSGSPETSAAAIMLLTVRHGTVRYRSSA LLARTKNNIQR YFGTNSVICSKKDKQSVRTEETS KETSESQDSEKENTKKDLLGIKGMKVELSTVNV RTTKPPKRRPLKSLEATLGRLRRATEYAPKKRIEP LSPELVAAASAVADSLPFDKQTTKSELLSQLQQH EEESRAQRDAKRPKISFSNIISDMKVARSATARV RSRPRLRIQFDEGYDNYPGQEKTDLLKKRKNIFT GKRLNIFDMMAVTKEAPETDTSPSLWDVEFAKQ LATVNEQPLQNGFEELIQWTKGKLWEPINNEA GFDDDGSEFHEHIFLEKHLESFPGQPIRHFMEVL TCGLSKNPYLSVKQKVEHIEWFRNYFNEKKDILK ESNIQFKLRPWKFLFRNN
3579	A	1725	445	RPRRRGTHHFSCVLGSFRVSAMFPRVSTFLPLRP LSRHPLSSGSPETSAAAIMLLTVRHGTVRYRSSA LLARTKNNIQR YFGTNSVICSKKDKQSVRTEETS KETSESQDSEKENTKKDLLGIKGMKVELSTVNV RTTKPPKRRPLKSLEATLGRLRRATEYAPKKRIEP LSPELVAAASAVADSLPFDKQTTKSELLSQLQQH EEESRAQRDAKRPKISFSNIISDMKVARSATARV RSRPRLRIQFDEGYDNYPGQEKTDLLKKRKNIFT GKRLNIFDMMAVTKEAPETDTSPSLWDVEFAKQ LATVNEQPLQNGFEELIQWTKGKLWEPINNEA GFDDDGSEFHEHIFLEKHLESFPGQPIRHFMEVL TCGLSKNPYLSVKQKVEHIEWFRNYFNEKKDILK ESNIQFKLRPWKFLFRNN
3580	A	3673	1619	LYCVAPYSRHLGRMSHLPKMLLRKKIEKRNK LRQRNLKFQGASNLTLSETQNGDVSEETMGSRK VKKSKQKPMNVGLSETQNGGMSQEA VGNIKVT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KSPQKSTVLTNGEAMQSSNSESKKKKKKKRRK MVNDAEPDTKKAKTENKKGKSEEEAETTKETEN NVEKPDNDEDESEVPSLPLGLTGAFEDTSFASLC NLVNENTLKAIKEMGFTNMTEIQHKSIRPLEGR DLLAAAKTGSGKTLAFLIPAVELIVKLRFMPRNG TGVLLSPTRELAMQTFGVLELMTHHVHTYGLI MGGSNRSAEAQKLGNGINIIVATPGRLLDHMQN TPGFMYKNLQCLVIDEADRLDVGFEELKQIIKL LPTRRQTM LFSATQTRKVEDLARISLKEPLYVG VDDDKANATVDGLEQGYVVCPEKRFLLLFTFL KKNRKKKLMVFFSSCMSVKYHYELLYNIDLPVL AIHGKQKQNKRTTTFQFCNADSGTLLCTDVA RGLDIPEVDWIVQYDPPDDPKEYIHRVGR TARGL NGRGHALLILRPEELGFLRYLKQSKVPLSEFDFS WSKISDIQSLEKLEKNYFLHKSQAQAYKSYIRA YDSHSLKQIFNVNNLNL PQVALSFGFKVPPFVDL NVNSNEGKQKKRGGGGGFGYQKTKKVEKSKIF KHISKSSDSRQFSH
3581	A	23	453	LCRCICIKNITPHCLWDKVL SQFTYILDNLSNFM HHPHSLRNSCLIRMDLLYWQFTIYTITFCFSLSG RLTLAQHISHRPCLLSYLLFWKVHHLFLEGFP SPRLDEMSFHQFPQHPVHVSVVHLPIVYKGSMT QVSPH
3582	A	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEA GIEAVGSAAEKGGVSDAYGEDDFSRLGGDED GYEEEEEDENSRQSEDDDDSETEKPEADDPKDNT AEKRDPQELVASFSEVRNMSPDEIKIPPEPPGRC SNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRN PSIYEKLIQFCAIDELGTNYPKDMFDPHGWSEDS YYEALAKAQKIEMDKLEKAKKERTKIEFVTGK KGTTTATSTTTTTASTAVADAQKRKSKWDSAI PVTIAQPTILTTTATLPAVVTVTTSASGSKTTVIS AVGTIVKKAKQ
3583	A	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEA GIEAVGSAAEKGGVSDAYGEDDFSRLGGDED GYEEEEEDENSRQSEDDDDSETEKPEADDPKDNT AEKRDPQELVASFSEVRNMSPDEIKIPPEPPGRC SNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRN PSIYEKLIQFCAIDELGTNYPKDMFDPHGWSEDS YYEALAKAQKIEMDKLEKAKKERTKIEFVTGK KGTTTATSTTTTTASTAVADAQKRKSKWDSAI PVTIAQPTILTTTATLPAVVTVTTSASGSKTTVIS AVGTIVKKAKQ
3584	A	3	1139	PGSTISSRADRLGAPVLAHPKMAERQEEQRGSP LRAEGKADAEVKLILYHWTHSFSSQKVRLVIAE KALKCEEHDVSLPLSEHNEPWFMRNLNSTGEVPV LIHGENIICEATQIIDYLEQTFLDERTPRLMPDKES MYYPVQHYRELDSLPMDAYTHGCILHPELTV DSMIPAYATTRISQIGNTESELKKLAENPDQ AYIAKQKRLKSKLLDHDNVKYLKILDELEKVL DQVETELPRRNEETPEEGQPWLCGESFTLADVS LAVTLHRLKFLGFARRNWGNKRPNLETYYERV LKRKTFNKVLGHVNNILISAVLPTAFRVAKKRAP KVLGTTLVVGLLAGVGYFAFMLFRKRLGSMILA LRPRPNYF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3585	A	1	1777	RRHSPGSPAFAPSSRATAICPRAARAPATLLLALG AVLWPAAGAWELTILHTNDVHSRLEQTSSESSK CVNASRCMGGVARLFTKVQQIRRAEPNVLLDA GDQYQGTIWFVTVYKGA EVAHFMNALRYDAMA LGNHEFDNGVEGLIEPLLKEAKFPILSANIKAKGP LASQISGLYLPYKVLPVGDEVVGVGYTSKETPF LSNPGTNLVFEDEITALQPEVDKLKTLNVNKIAL GHSGFEMDKLIAQKVRGVDVVVGHSNTFLYT GNPPSKEVPAGKYPFIVTSDDRKVPVQAYAF GKYLGYLKIEFDERGNVISSHGNPILLNSSIPEDPS IKADINKWRIKLDNYSTQELGKTIVYLDGSSQSC RFRECNMGNLICDAMINNNLRHTDEMFWNHVS MCILNGGGIRSPIDERNNGTITWENLA AVL PFGG TFDLVQLKGSTLKKAFEHSVHRYGQSTGEFLQV GGIHVVYDLSRKPGDRVVKLDVLC TKRVP SYD PLKMDEVYKVILPNFLANGDGFQMIKDELLRH DSGDQDINVVSTYISKMKVIYPAVEGRIKFSTGS HCHGSFSLIFLSLWAVIFVLYQ
3586	A	1399	881	LSNKDVLSPQLKDENSEKLRRLNEVQSFSEAQTE MVRTLERKLEAKMIKEESDYHDLSEVVQQVEQN LELMTKRAVKAENHVVKLQKEISLLQAQVSNQ RENEALRCGQGASLTVVKQNADVALQNLRVVM NSAQASIEQLVSGAETLNLVAEILKSIDRISEVKD EEEDS
3587	A	88	1639	GCVGRGLPLPPRHPTPPSSSSSPFVLLAFLLVRL DPAVSGKMAAPRPPPARLSGVMVPAPIQDLEAL RAL TALFKEQRNRETAPRTIFQRVLDILKKSSHA VELACRDPSQVENLASSLQLITECFRCLRNACIEC SVNQNSIRNLDTIGVAVDLILLFRELRVEQESLLT AFRCGLQFLGNIASRNEDSQSIVWVHAFPELFLS CLNHPDKKIVAYSSMILFTSLNHERMKELEENLN IAIDVIDAYQKHPESEWPFLIITDLFLKSPELVQA MFPKLNQERVTLDDLMIAKITSDEPLTKDDIPVF LRHAELIASTFVDQCKTVLKLASEEPPDDEEALA TIRLLDVLCMTVNTTELLGYLQVFPGLLERVIDL LRVIHVAGKETTNIFSNCGCVRAEGDISNVANGF KSHLIRLIGNLCYKNKDNQDKVNELDGIPLILDN CNISDSNPFLTQWVIYAIRNLTEDNSQNQDLIAK MEEQGLADASLLKKVGFEVEKKGEKLILKSTRD TPKP
3588	A	3	1462	DSPNRNFEILGRPTRTPTRPGPRPAMEDLDALLSD LETTTSHMPRSGAPKERPAEPLTPPSYGHQPQT GSGESSGASGDKDHLYSTVCKPRSPKPAAPAAPP FSSSSGVLGTGLCELDRLQLNELNATQFNITDEIMS QFPSSKVASGEQKEDQSEDKKRPSLPSSPSPGLPK ASATSATLELDRLMASLSDFRVQNHLPASGPTQP PVVSSSTNEGSPSPPEPTGKGS LDTMLGLLQSDLSR RGVPTQAKGLCGSCNKPIAGQVV TALGRAWHPE HFVCGGCSTALGGSSFEKDGAPFCPECYFERFSP RCGFCNQPIRHKMVTALGTHWHPEHFCVSCGE PFGDEGFHEREGRPYCRRDFLQLFAPRCQGCQGP ILDNYISALSALWHPDCFVCRECFAPFSGGSFFE EGRPLCENHFHARRGSLCATCGLPVTGRCVSAL GRRFHPDHFTCTFCLRPLTKGSFQERAGKPYCQP CFLKLF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3589	A	226	6793	SPPKKSRLCNLSFRLISAERWRFFLLILMEMPRKP RLTLFVQRRRIENIATEREFDPEEFYLLLEAAEGHA KEGQGIKTDIPRYIISQLGLNKDPLEEMAHLGNY DSGTAETPETDESVSNNASLKLRRKPRESDFETI KLISNGAYGAVYFVRHKEQRQFAMKKINKQNL ILRNQIQQAFVERDILTFAENPFVSMYCSFETRR HLCMVMEYVEGGDCATLMKNMGPLPVDMAARM YFAETVLALEYLHNYGIVHRDLKPDNLLVTSMG HIKLTDFGLSKVGLMSMTTNLYEGHIEKDAREFL DKQVCGTPEYIAPEVILRQYGKPVDDWWAMGII LYEFVLGCVPFPGDTPEELFGQVISDEINWPEKDE APPPDAQDLITLLLRQNPLERLGTGGA YEVKQHR FFRSLDWNSSLRQKAEIFPQLESEDDTSYFDTRSE KYHHMETEEEDDTNDEDFNVEIROFSSCSHRFSK VFSSIDRITQNSAEEKEDSVDKTKSTTLPTSTETLS WSSEYSEMQLSTSNSSDTESNRHLSSGLLPKL AISTEGEQDEAASCPGDPHEEPGKPALPPEECAQ EEPEVTPASTISSSTLSVGSFSEHLDQINGRSECV DSTDNSSKPSSEPASHMARQRLESTEKKISGKV TKSLASALSMLPGDMFAVSPLGSPMSPHLSDD PSSRDSSPSRDSSAASAPHQPIVHSSGKNYGFT IRAIRVYVGDSDIYTVHHIVWNVEEGSPACQAGL KAGDLITHINGEPVHGLVHTEVIELLLKSGNKVSI TITPFENTSIKTGPARRNSYKSRMVRRSKSKKK ESLERRRSLFKKLAKQPSPLLHTSRFSCLNRSLS SGESLPGSPHSLSPRSTPSYRSTPDFPSGTNNSQ SSSPSSAPNSPAGSGHIRPSTLHGLAPKLGGQRY RSGRRKSAGNIPLSPLARTPSPTPQTPSPQRSPL LGHSLGNSKIAQAFPSKMHSPPTIVRHIVRPKSAE PPRSPLLKRVQSEKLSPSYGSDDKKHLCSRKHSL EVTQEEVQREQSQREAPLQSLDENVCVPLPSRA RPVEQGCLKRPVSRKVGRQESVDDLDRLDKLAK VVVKKADGFPEKQESHQKFHGPBGSDLENFALFK LEEREKKVYPKAVERSSTFENKASMQEAPPLGSL LKDALHKQASVRASEGAMSDGPVPAEHRQGGG DFRRAPAPGTLQDGLCHSLDRGISGKGEGTEKSS QAKELLRCEKLDKLANIDYLRKKMSLEDKEDN LCPVLKPKMTAGSHECLPGNPVRPTGGQEQEPPPA SESRAFVSSTHAAQMSAVSFVPLKALTGRVDSGT EKPGLVAPESPVRKSPSEYKLEGRSVSCLEPIEGT LDIALLSGPQASKTELPSPESAQSPSPSGDVRASV PPVLPSSSGKKNDTTSARELSPSSLKMNKSYLLEP WFLPPSRGLQNSPAVSLPDEPKRDRKGPHPTAR SPGTVMESNPQOREGSSPKHQDHTTDPKLLTCLG QNLHSPDLARPRCPLPPEASPSREKPGRESSERG PPTARSERSAARADTCREPSMELCFPETAKTSDN SKNLLSVGRTHPDFYTQTQAMEKAWAPGGKTN HKDGPGEARPPRDNSSLHSAGIPCEKELGKVRR GVEPKPEALLARRSLQPPGIESEKSEKLSFSPSLQ KDGAKEPERKEQPLQRHPSSIPPPPLTAKDLSSPA ARQHCSSPSHASGREPGAKPSTAEPSSSPQDPPKP VAAHSESSSHKPRPGPDGPPKTKHPDRSLSSQK PSVGATKGKEPATQSLGGSSREGKGHSKSGPDVVF PATPGSQNKASDGIGQGEGGPSVPLHTDRAPLDA KPQPTSGRPLEVLEKPVHLPRPGHPGPSEPADQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KLSAVGEKQTLSPKHPKPSTVKDCPTLCKQTDN RQTDKSPSPQAANTDRRAEGKKCTEALYAPAEG DKLEAGLSFVHSENRLKGAERPAAGVGKGFPEA RGKGPQPKPTEADKPNGMKRSPSATGQSSFRS TALPEKSLSCSSSPETRAGVREASAASDSTSSAK AAGGMLELPAPSNRDHRKAQPAGEGRTHMTKS DSLPSFRVSTLPLESHHPDPNTMGGASHRDRALS VTATVGETKGKDPAPAQPPARKQNVGRDVTKP SPAPNTDRPISLSNEKDFVVRQRRGKESLRSSPHK KAL
3590	A	3	935	RATTPKNEVQDYVSVEYLSPHMGGTDPFKYSY PPLVDDDFQTPLCENGPISEDETSSKEDIESDGK ETLETISNEEQTPLLKKINPTTESTSKAEENEKVDS KVKAFFKKPLSVFKGPLLHISPAEELYFGSTSEGEK KTLIVLTNVTKNIVAFKVRTTAPEKYRVKPSNSS CDPGASVDIVVSPHGGGLTVSAQDRFLIMAAEME QSSGTGPAELTQFWKEVPRNKVMEHRLRCHTVE SSKPNTLTLKDNAFNMSDKTSEDICLQLSRLLES NRKLEDQVQRQIWFQQLLSLTMLLLAFVTSFFY LLYS
3591	A	303	2	GGSWGPLCPVSPAMSLSDPGLGYHPTCWTLRWP PLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCS CEAGGSCACAGSCKCKCKCTSCCKSCCSCCPL
3592	A	1052	1779	GKTMMRKMLLAAALSVTAMTAHADYQCSVTP RDDVIVSPQTVQVKGENGNLVITPDGNVMYNGK QYSLNAAQREQAKDYQAE LRSTLPWIDEGAKSR VEKARIALDKIIVQEMGESSKMRSRLTKLDAQVK EQMNRIETRS DGLTFHYKAIDQVRAEGQQLVNQ AMGGILQDSINEMGAKAVLKSGGNPLQNVLGSL GGLQSSIQT EWKKQEKDFQQFGKDVCSRVTLE DSRKALVGNLK
3593	A	3	1837	LSFEKVDIQTNDLTKEMYEGKENVSFELQRDFS QETDFSEASLLEKQQEVHSAGNIKKEKSNTIDGT VKDETSPVEECFFSQSSNSYQCHTITGEQPSGCTG LGKSISFDTKLVKHEINSEERPFKCEELVEPFRC SqliQHqENNTeeKPYQCSECGKAFSINEKLIWH QRLHSGEKPFCVECGKSFSYSSHYITHQTHSGE KPYQCKMCGKAFSVNGSLSRHQRIHTGEKPYQC KECGNGFSCSSAYITHQRVHTGEKPYECNDCGK AFNGNAKLIQHQRHTGEKPYECNECGKGFRCS QLRQHQSHTGEKPYQCKEKGKGFNNNTKLIQH QRIHTASLAEQLFKASGNHPNWGCCLTISSPGPS VYGPKMNMARGAPNSRLAGGREKRTQDTDFGQC SFLPSHSPSCFEPWNVTDYDSSWYRQKQVLSGV WSSPLSILKLPRTLIRISIHQEMDTPGEMLMTGR GSLGPTLTTEAPAAQPGKQGPPTGRCLQAPGT EPGEQTPEGARELSPLQESSSPGGVKAEEEQRAG AEPGTRPSLARSDNDHEVGALGLQQGKSPGAG NPEPEQDCAARAPVRAEAVRRMPPGAEAGSVVLD DD
3594	A	39	261	RAAMMDTSRVQPIKLAIVIKVLGRTGSQGQCTQ VRVEFMDDTSRSIIRSVKGPVREGDVLTLLESERE ARRLR
3595	A	973	68	GRVGTKHQMADDAGAAGGPGGPGGPGMGNRG GFRGGFGSGIRGRGRGRGRGRGRGARGGKAE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DKEWMPVTKLGRLVKDMKIKSLEEIYLFSLPIKE SEIIDFFLGASLKDEVLKIMPVQKQTRAGQRTRF KAFVAIGDYNHGVGLGVKCSKEVATAIRGAILLA KLSIVPVRRGYWGNKIGKPHTVPCKVTGRCGSV LVRLIPAPRGTGIVSAPVPKLLMMAGIDDCYTS ARGCTATLGNFAKATFDAISKTYSYLTPDLWKE TVFTKSPYQEFTHLVKTHTRVSVQRTQAPAVA TT
3596	A	106	2960	DERRVGAADMFGRSRSWVGGGHGTSTSRNIHSL DHLKYLHVLTNTTVTEQNRNLLVETIRSITEIL IWGDQNDSSVDFDFLEKNMFVFFLNILRQKSGRY VCVQLLQTLNLFENISHETSLYYLLSNVYVNSII VHKFDFSDEEIMAYYISFLKTLCLKNNHTVHFF YNEHTNDFALYTEAIKFFNHPESMVRIVRTITL NVYKVSLEDNQAMLHYIRDKTAVPYFSNLVWFIG SHVIELDDCVQTDDEHRNRGKLSDLVAEHLDDL HYLNDILINCEFLNDVLTDLHLLNRLFLPLVYVSL ENQDKGGERPKISLPVSLYLLSQVFLIIHHAPLVN SLAEVILNGDLSEMYAKTEQDIQRSSAKPSIRCFI KPTETLERSLEMNKHKGKRRVQKRPYKNVGE EDEEKGPTEDAQEDA EKA KGTGGSKGIKTSGES EEIEMVIMERSKLSELAASTSVQEONTTDEEKS AATCESTQWSRPFLDMVYHALDSPDDDYHALF VLCLLYAMSHNKGMDPEKLERIQLPVPNAAEKT TYNHPLAERLIRIMNNAAPDGKIRLATLELSCL LLKQQVLM SAGCIMKDVHLACLEGAREESVHLV RHFYKGEDIFLDMFEDEYRSMTMKPMNVEYLM MDASILLPPTGTPLTGIDFVKRLPCGDVEKTRAI RVFFMLRSLSLQLRGEPETQLPLTREEDLIKTDV LDLNNSDLIACVTITKDGGMVQRSLAVDIYQMS LVEPDVSR LGWGVVKFAGLLQDMQVTGVEDDS RALNITHKPASSPHSKPFILQATFIFSDHIRCIAK QLAKGRIQARRMKMQRIAALLDLPIQPTTEVLG FGLGSSTSTQHLPRFYDQGRRGSSDPTVQRSVF ASVDKVPGFVAQCINEHSSPSLSSQSPSASGSP SGSGSTSHCDSGGTSSSSTPSTAQSPAGIGHVTQ
3597	A	427	277	GVRRIQHWAQMHECNVHTYASLFLCLLHTG KLCCLNHRHFHCIKYSK
3598	A	1	503	FRPRTKKATAMYLEHYLDSIENLPCELQRNFQL MRELDQRTEDKKA EIDILAAEYISTVKTLSPDQR VERLQKIQNAYSKCKEYSDDKVQLAMQTYEMV DKHIRRLDADLARFEADLKDKMEGSDFESSGGR GLKKGRGQKEKRGSRGRGRRTSEEDTPKKKKH KGG
3599	A	2	3907	KTITALAFSPDGKYLVTGESGHMPAVRVWDVAE HSQVAELQEHKYGVACVAFSPSAKYIVSVGYQH DMIVNVWA WKKNIVVASNKVSSRVTAVSFSED CSYFVTAGNRHIKFWYLD DSKTSKV NATVPLL RSGLLGELRNNLFTDVACGRGKKADSTFCITSSG LLCEFSRRLLDK WVELRVYPEVKDSNQACLPP SSFITCSSDNTIRLWNTESSGVHGSLHRNLSSDL IKIYYVDGNTQALLDTLP GGDKADASLLDPRVGI RSVCVSPNGQH LASGDRMGTLRVHELQSLSEML KVEAHDSEILCLEYSKPD TGLKLLASASRDLIH VLDAGREYSLQQTLDEHSSSITAVKFAASDGQVR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				MISCGADKSIYFRTAQKSGDGVQFTRTHHVVRK TTLYDMDVEPSWKYTAIGCQDRNIRIFNISSGKQ KKLFKGSQGEDGTLIKVQTDPSGIYIATSCSDKNL SIFDFSSGECVATMFGHSEIVTGMKFSNDCKHLIS VSGDSCIFVWRLSSEMTISMQRQLAELRQRQGG KQQGPSSPQRASGPNRHQAPSMLSPGPALSSDS KEGEDEGTEELPALPVLAKSTKKALASVPSPAL PRSLSHWEMSRAQESVGFLDPAPAAPNGPRRRG RWVQPGVELSVRSMLDLRQLETAPSLQDPSQD SLAIPSGPRKHGQEALETSLTSQNEKPPRPQASQ PCSYPHIIRLLSQEEGVFAQDLEPAPIEDGIVYPEP SDNPTMDTSEFQVQAPARGTLGRVYPGSRSSSEK HSPDSACSVDYSSSCLSSPEHPTDESSETEPLSVD GISSDLEEPAEGDEEEEEEGGMGPYGLQEGSPQ TPDQEQFLKQHFETLASGAAPGAPVQVPERSESR SISSRFLLQVQTRPLREPSSSSSSLALMSRPAQVPQ ASGEQPRGNGANPPGAPPEVEPSSGNPSPQQAAS VLLPRCRLNPDSSWAPKR VATASPFSGLQKAQS VHSLVPQERHEASLQAPSPGALLSREIEAQDGLG SLPPADGRPSRPHSYQNPTTSSMAKISRISVGEN LGLVAEPQAHAPIRVSPLSKLALPSRAHLVLDIPK PLPDRPTLAASFSPVTKGRAPGEAEKPGFPVGLGK AHSTTERWACLGEGETPKPRTECQAHGPGSSPCA QQLPVSSLFQGPENLQPPPEKTPNPMECTKPGA ALSQDSEPAVSLEQCEQLVAELRGSVRQAVRLY HSVAGCKMPSEAEQSRIAQLLRDTFSSVRQELEAV AGAVLSSPGSSPGAVGAEQTQALLEQYSELLRA VERRMERKL
3600	A	1688	916	IPGSTISCSMALCEAAGCGSALLWPRLLLFGDSIT QFSFQGGWGASLADRLVRKCDVLNRGFSGYN TRWAKIILPRLIRKGNLSDIPVAVTIFFGANDSAL KDENPKQHIPLEEY AANLKS MVQYLKSV DIPENR VILITPTPLCETA WEEQCHIQGCKLNRLNSVVGEY ANACLQVAQDCGTDVLDLWTLMQDSQDFSSYL SDGLHLSPKGNEFLFSLWPLIEKKVSSLPLLLPY WRDVAEAKPELSLLGDGDH
3601	A	44	223	VHFPLIPQLAKCFWTMNRARNKSEKRY YSEFL QIAHLFNYGLSSFLREFIIFLIKLLQ
3602	A	37	1124	VPKPASGKRRLEFRPQDSKACAATPHSPGRITSR TRGSQKVRSVPPRLPWAQASASTDWEGLRGVPG PALRRENFLA AASGRSGRTPTGGVGFRDVGGP HFPIFPAAHFLWCNLHTPRRPACNAPWHSPVGEI SPPPRESQLRRDPEVHFESPAHPLGFRLLPGRGLP ANAVTVETAAMAAPRQIPSHIVRLKPSCTDSSF TRTPVPTVSLASREL PVSSWQVTEPSSKNLWEQI CKEYEA EQPPFPEG YKVKQEPVITVAPVEMLFH GFSAEHYFPVSHFTMISRTPCPQDKSETINPKTCS PKEYLET FIFPVLLPGMASLLHQA KKEKCFEVL QMTPSGGKACVWGHLPSSSHTI
3603	A	286	587	NISNKA EVSSHPSVISHSMDSFGQPRPEDNQSVLR RMQKKYWKTKQVFIKATGKKEDEHLVASDAEL DAKLEVFHSVQETCTELLKIEKYQLRLNGMKS
3604	A	103	2440	QPRRRVFPAAGRGPGRKCSQWGRQASVSFEDVT VDFSKEEWQHLDPAQRRLYWDVTLNYSLLS VGYQIPKSEAFKLEQGEGP WMLEGEAPHQSCS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GEAIGKMQQQGIPGGIFFHCERFDQPIGEDSLCSI LEELWQDNDQLEQRQENQNNLLSHVKVLIKERG YEHKNIEKIIHVTTKL VPSIKRLHNCDTILKHTLN SHNHNRRNSATKNLGKIFGNNGNPFHSPSSSTKNEN AKTGANSCEHDHYEKHL SHKQAPTHHQKIHPEE KLYVCTECVMGFTQKSHLFEHQRIHAGEKSREC DKSNKVFPQKPQVDVHPSVYTGEKPYLCTQCGK VFTLKS NLITHQKIHTGQKPYKCSECGKAFFQRS DLFRHLRIHTGEKPYECSECGKGFSQNSDL SIHQ KTHTGEKHYECNECGKAFTRK SALRMHQRIHTG EKPYVCADCGKAFIQKSHFNTHQRIHTGEKPYEC SDCGKSFTTKSQLHVHQRIHTGEKPYICTECGKV FTHRTNLTTTHQKTHTGEKPYMCAECGKAFTDQS NLIKHQKTHTGEKPYKCNGCGKAFIWKSR LKIH QKSHIGERHYECKDCGKAFIQKSTLSVHQRIHTG EKPYVCPEGKAFIQKSHFIAHHRHTGEKPYECS DCGKCF TKKSQLRVHQKIHTGEKPNICAECGKAF TDRSNLITHQKIHTREKPYECGDCGKTFTWKSRL NIHQKSH TGERHYECSKCGKAFIQKATLSMHQII HTGKKPYACTECQKAFTDRSNLIKHQKMHSGEK RYKASD
3605	A	3	322	SFRMSGRGKGGKGLGKGGAKRHRKVLRDNIQGI TKPAIRRLARRGGVKRISGLIYEETRGVLKVLEN VIRDAVTYTEHAKRKTVTAMDVVYALKRQGR LYGFGG
3606	A	1	1749	VPVTAEAKLMGFTQGCVT FEDVAIYFSQEEWGL LDEAQRLLYRDVMLENFALITALVCWHGMEDE ETPEQSVSVEGV PQVRTPEASPTQKIQSCDMCV PFLTDILHLTDLPQQLYLTGACAVFHQDQKHHS AEKPLESDMDKASFVQCCLFHESGMPFTSSEVG KDFLAPLGILQPQAIANYEKP NKISKCEEAFHVG SHYKWSQCRRESSHKHTFFHPRVCTGKRLYESS KCGKACCCECSLVQLQRVHPGERPYECSECGKS FSQTSHLNDHRRHTGERPYVCGQC GKSFQRAT LIKHHRVHTGERPYECGECGKSFSQSNLIEHCRI HTGERPYECDECGKAFGSKSTLVRHQRTHTGEK PYECGECGKLFRQSFSLVVHQRIHTTARPYECGQ CGKSFS LKCGLIQHQLIHSGARPFECDECGKSFSQ RTTLNKH HKVHTAERP YVCGECGKAFMFKSKL VRHQRTHTGERPFECSECGKFFRQSYTLVEHQKI HTGLRPYDCGQC GKSFQKSSLIQHQQVHTGERP YECGKCGKSFTQHSGLILHRKSHTVERPRDSSK GKPYSPRSNIV
3607	A	92	331	AMAGPGPGPDPEQYDFLKLVLVG DASVGKT CVVQRFKTGAFSERQGSTIGVDFTMKLTLEIQGR VKLQIWDTAGQR
3608	A	545	379	AIKGYIHLSAPRNR YMHTTASNGRMLFMKV TM YMRRGVQIMGWSVRMAFMACFTQ
3609	A	118	873	VWMAWQVS LLELEDRLQCPICLEVFKE SMLQC GHSYCKGCLVSLSYHLDTKVRCPMCWQVVDGS SSLPNVSLA WVIEALRLPGDPEPKVCVHHRNPLS LFCEKDQELICGLGGLGSHQHHPVTPVSTVCSR MKEELAA LFSSELKQE QKKVDELI AKLVKNRTRIV NESDVFSWVIRREFQELRHPVDEEKARCLEGIGG HTRGLVASLDMQLEQAQGTRERLAQAECVLEQF

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GNEDHHEFIWKFHSMASR
3610	A	2	987	DPRVRPPLLQPPPLLPRLVILKMAPLDDLDKYVEI ARLCKYLPENDLKRCLCDYVCDLLEESNVQPV TPVTVCGDHGGFYDLCELFRTGGQVPDNYIFM GDFVDRGYYSLETFTYLLALKAKWPDRTLLRG NHESRQITQVYGFYDECQTKYGNANAWRYCTK VFDMLTVAALIDEQILCVHGGGLSPDIKTLQIRTI ERNQEIPHKGAFCDLVWSDPEDVDTWASPRGA GWLFGAKVTNEFVHINNKLICRAHQLVHEGYK FMFDEKLVTVWSAPNYCYRCGNIASIMVFKDVN TREPCLFRAVPDSERVIPRTTTPYFL
3611	A	2459	869	AEKMTAELREAMALAPWGPVKVKKEEEEEENF PGQASSQVHSENIKVWAPVQGLQTGLDGSEEE EKGQNISWDMAVVLKATQEAPAASTLGSYSLPG TLAKSEILETHGTMNFLGAETKNLQLLVPKTEIC EEAEKPLIISERIQKADPQGPPELGEACEKGNMLK RQRIKREKKDFRQVIVNDCHLPESFKEEENQKCK KSGGKYSLSNGAVKNPKTQLGQKPFTCSVCGKG FSQSANLVVHQRIHTGEKPFECHECGKAFIQSAN LVVHQRIHTGQKPYVCSKCGKAFQSSNLTVHQ KIHSLEKTFKCNECEKAFSYSSQLARHQKVHITE KCYECNECGKTFTRSSNLIVHQRIHTGEKPFACN DCGKAFQSANLIVHQRSHTEKPYECKEKGKA FSCFSLIVHQRIHTAEKPYDCSECGKAFSLSCL IVHQRIHSGDLVVCNECGKAFQSSYLLIHQRIH NGEKPYTCNECGKAFRQRSSLTVHQRTHTGEKP YECEKCGA AFISNSHLMRHHRTHLVE
3612	A	318	2245	SPMAEAAALVNTQPIMVTEEFVKPSQGHVTFEDI AVYFSQEEWGLLDEAQRCLYHDMLENFSLMA SVGCLHGIEAEEAPSEQTLAQQVVSQARTPKLGP SIPNAHSCMCILVMKDILYLSEHQGTLPWQKPY TSVASGKWFSFGSNLQQHQNQDSGEKHIREESS ALLNSCKIPLSDNLFCKDVEKDFPTILGLLQHQ TTHSRQEYAHRSRETFQRRYKCEQVFNEKVHV TEHQRVHTGEKAYKRREYKSLNSKYLFEVHQ THNAEKPYVCNICGKSFLHKQTLVGHQQRIHTRE RSYVCIECGKSLSSKYSLEHQRTHNGEKPYVCN VCGKSFRHKQTFVGHQQRIHTGERPYVCMCEGK SFIHSYDRIRHQRVHTGEGAQCSECGKSFIYKQ SLLDHHRHTGERPYECKEKGKAFIHKRLLHEHQ RIHTGEKPYVCIICGKSFISSDYMRHQRIHTGER AYECSDCGKAFISKQTLKHHKIHTRERPYECSE CGKGFYLEVKLLQHQRHTREQLCECNECGKVF SHQKRLLHEQKVHTGEKPECECGKCFRHRSTS LIQHQQVHSGERPYNCTACEKAFIYKNKLVEHQ RIHTGEKPYECGKCGKAFNKRYSLVRHQKVHIT EEP
3613	A	817	3345	NQSHPDSETVTVEGGRRKMKSNOQRSNECLPPK KREIPATSRSEEKAPTLPSDNHRVEGTAWLPGN PGGRGHGGGRHGPAGTSVELGLQQGIGLHKALS TGLDYSPPSAPRSVPVATTLPAAYATPQGTVPSP VQYAHLPHTFQFIGSSQYSGTYASFIPSQLIPTAN PVTSASASAAGATTPSQRSQLEAYSTLLANMGS LSQTPGHKAEQQQQQQQQQQQQQQQQQQQQQQ QQQHQQQQQQQQQQQQQQQQHLSRAPGLITPGSP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				PAQQNQYVHISSSPQNTGRTASPPAIPVHLHPHQ TMIPHTLTGPPSQVVMQYADSGSHFVPREATK KAESSRLQQAIAKEVLNGEMEKSSRRYGAPSSA DLGLGKAGGKSVPHPYESRHVVVHPSPSDYSSR DPSGVRASVMVLPNSNTPAADLEVQQATHREAS PSTLNDKSGHLGKPGHRSYALSPHTVIQTTTHSA SEPLPVGLPATAFYAGTQPPVIGYLSGQQQAITY AGSLPQHLVIPGTQPLLIPVGSTDMEASGAAPAIV TSSPQFAAVPHTFVTTALPKSENFNPEALVTQAA YPAMVQAQIHLVVVQS VASPAAPPTLPPYFMK GSHQLANGELKKVEDLKTEDFIQSAEISNDLKIDS STVERIEDSHSPGVAVIQFVGEHRAQVSVEVLV EYPPFFVFGQGWSSCCPERTSQLFDLPCSKLSVGD VCISLTLKNLKNKSGVKKGQVPDPASVLLKHSKA DGLAGSRHRYAEQENGINQGSQAQMLSENGELKF PEKMGLSAAPFLTKIEPSKPAATRKRRWSAPESR KLEKSEDEPPLTLPKPSLIPQEVKICIEGRSNVVGK
3614	A	3	114	FFESRLRCKCCEPRGSWARFGCWRLQPEFKPKQ LEG
3615	A	3	1603	DAWALTNQFSDSKQHIEVLKESLTAKEQRAAILQ TEVDALRLREEKETMLNKKTKQIQDMAEEKGT QAGEIHDLDKMDLVKERKVNVLQKKIENLQEQ RDKEKQMSSLKERVKSQADTTNTDTALTLEE ALAEKERTIERLKEQRDRDEREKQBEIDNYKKDL KDLKEKVSLLQGDLSKEASLLDLKEHASSLASS GLKKDSRLKTLLEIALEQKKEECKMESQLKKAH EAALEARASPEMSDRIQHLEIRETRYKDESSKAQ AEVDRILLEILKEVENEKNDKDKIAELESLSRQ VKDQNKKVANLKHKEQVEKKKSAQMLEEARRR EDNLDSSQQLQDSLKKDDRIEELBEALRESVQ ITAEREMVLAQESARTNAEKQVEELLMAMEKV KQELESMAKLSSTQQSLAEKETHLTNLRAERR KHLEEVLEMKQEALLAAISEKDANIALLELSSSK KKTQEEVAALKREKDRLVQQLKQQTQNRMKLM ADNYEDDHFKSSHSNQTNHKPSPDQDEEGIWA
3616	A	244	1420	RRRWRARGGLVPTLAWAEATGAYVPGRDKPD PTWKRNFRLNRKEGLRLAEDRSKDPHDPHI YEFVNSGVGDFSQPDTSPTNNGGSTSDTQEDIL DELLGNMVLAPLPDPPSLAVAPEPCPQLRSPS LDNPTFPNLPSENPLKRLVPGEEWEFEVTA YRGRQVFQQTISCPEGLRLVGSEVGDRTLP VTLPPGMSLTDRGVMSYVRHVLSCGGGLAL WRAGQWLWAQRLGHCHTYWAVSEELLPSNGH GPDGEVPKDKEGGVFDLGPFI VGS LGPPDLIT FTE GSGRSPRYALWFCVGESWPQDQPWTKRLVMVK VVPTCLRALVEMARVGGASSENTVDLHISNSHP LSLTSDQYKAYLQDLVEGMDFQGPGES
3617	A	852	304	RGGLLSKMARVLKAAAANAVGLFSRLQAPIPTV RASSTSQPLDQVTGSVWNLGRLNHVAIAVPDLE KAAAFYKNILGAQVSEAVPLPEHGVSVFVNLG NTKMELLHPLGRDSPIAGFLQKNKAGGMHHICIE VDNINAAVMDLKKKKIRSLSEEVKIGAHGKPVIF LHPKDCGGVLVELEQA
3618	A	3	5992	DNIDETYGVNVQFESDEEEGDEDEVYGEVREEAS DDDMEGDEAVVRCTLSANMYVDEILVWCASEL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NIPEFFPLESPHKKVGYGLSSRTWLQGGGKVIEA GRDLLVASGELMSSKKKDLHPRDIDAFWLQRQL SRFYDDAIVSQKKADEVLEILKTASDDRECENQL VLLLGFTDFIKVLRQHRMMILYCTLLASAQSE AEKERIMGKMEADPELSKFLYQLHETEKEDLIRE ERSRRERVRQSRMDTDLETMDLDQGGGEALAPRQ VLDLEDLVFTQGSHFMANKRCQLPDGSFRRQRK GYEEVHVPALKPKPFGSEEQLLPVEKLPKYAQA GFEGFKTLNRIQSKLYRAALETDENLLLCAPTGA GKTINV ALMCMLEIGKHINMDGTINVDDFKIYI APMRSLVQEMVGSFGKRLATYGITVAELTGDHQ LCKEEISATQIVCTPEKWDIITRKGGERTYTQLV RLILDEIHLHDDRGVLEALVARAIRNIEMTQE DVRLIGLSATLPNYEDVATFLRVPKGLFYFDN SFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIM EHAGKNQVLVVFVHSRKETGKTARAIKDMCLEKD TLGLFLREGSASTEVLRTEAEQCKNLELKDLLPY GFAIHAGMTRVDRTLVEDLFGDKHIQVLVSTA TLAWGVNLPAAHTVIKGTQVVSPEKGRWTELGA LDILQMLGRAGRPQYDTKGEGLITSHGELQYYL SLLNQQLPIESQMVSKLPDMLNAEIVLGNVQNA KDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGD PLLDQRRDLVHTAALMLDKNNLVKYDKKTGN FQVTELGRASHYYITNDTVQTYNQLLKPTLSEIE LFRVFSLSSEFKNITVREEEKLQKLLERVIPVK ESIEEPSAKINVLLQAFISQLKLEGFALMADMVY VTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCK MIDKRMWQSMCPLRQFRKLPEEVVKKIEKNFP FERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPK LELSVHLQPIRSTLKVELTITPDFQWDEKVBHSS EAFWILVEDVDSEVILHHEYFLKAKYAQDEHLI TFFVPVFEPLPPQYFIRVVS DRWLSCETQLPVSR HLILPEKYPPTELLDLQPLPVSA LRNSAFESLYQ DKFFFFNPIQTQVFNTVYNSDDNVFVGAPTGS GK TICAFAILRMLLQNSEGRVCYITPMRLWQE QVY MDWYEKFQDRLNKKVLLTGESTDLKLLGKG NIIISTPEKWDILSRRWKQRKNVQNINLFVVDEV HLIGGENGPVLEVICS RMRYISSQIERPIRIVALSSS LSNKDV AHWLGCSATSTFNHPNVRPVLELHI QGFNISHTQTRLLSMAKPVFHAITKHSPKKPVIVF VPSRKQTRLTAIDILTTCAADIQRQFLHCTEKDL IPYLEKLSDSLKETLLNGVGYLHEGLSPMERRL VEQLFSSGAIQVVVASRSLCWGMNVA AHLVIIM DTLYYNGKIHAYVDYPIYDVLQMVGHANRPLQ DDEGRCVIMCQGSKKDFFKKFLYEPLPVESHLD HCMHDHFNAEIVTKTIENKQDAVDYLTWTFLYR RMTQNP NYNLQGISHRHLSDHLSSELVEQTLSDL EQSKCISIEDEM DVA PLNLGMIAAYYYNYTTIEL FMSLSNAKTKVRGLIEIISNAAYENIPIRHHEDN LLRQLAQKVPKLNPNPKFNDPHVKTNLLQAH L SRMQLSAELQSDTEILSKAIRLIQACVDVLSSNG WLSPALAAMELAQMVTQAMWSEDSYLRRLPPF PSGLFKRCTDKGVESVFDIMEMEDEERNALLQLT DSQIADVARFCNRYPNIELSYEVVDKDSIRSGGP VVVLVQLEREEEV TGPVIAPLFPQKREEGWVVV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				IGDAKSNSLSIKRLTLQQKAKVKLDFVAPATGGRHNTLYFMSDAYMGCDQEYKFSVDVKEAETDS DSD
3619	A	3	5992	DNIDETYGVNVQFESDEEEGEDVDYGEVREEAS DDDMEGDEAVVRCTLSANMYVDEILVWCASEL NIPEFFPLESPHKKVGYGLSSRTWLQGGGVIEA GRDLLVASGELMSSKKKDLHPRDIDAFWLQRQL SRFYDDAIVSQKKADEVLEILKTASDDRECENQL VLLGFNTDFIKVLRQHRMMILYCTLLASAQSE AEKERIMGKMEADPELSKFLYQLHETEKEDLIRE ERSRRERVRQSRMDTDLETMDLDQGGREALAPRQ VLDLEDLVFTQGSFHMANKRCQLPDGSFRRQRK GYEEVHVPALKPKPFGSEEQLLPVEKLPKYAQA GFEGFKTLNRIQSKLYRAALETDENLLCAPTGA GKTNVALMCMLEIGKHINMDGTINVDFFKIYI APMRSLVQEMVGSFGKRLATYGITVAELTGDHQ LCKEEISATQIIVCTPEKWDITRKGGERITYTQLV RLIILDEIHLHDDRGPVLEALVARAIRNIEMTQE DVRIGLSATLPNYEDVATFLRVDPAKGLFYFDN SFRPVPLEQTYVGITEKKAIKRFQIMNEIVYEKIM EHAGKNQVLVVFHSRKETGKTARAIKDMCLEKD TLGLFLREGSASTEVLRTEAEQCKNLELKDLLPY GFAIHHAGMTRVDRTLVEDLFGDKHIQVLVSTA TLAWGVNLPHTVVIKGTQVVSPEKGRWTELGA LDILQMLGRAGRPQYDTKGEGILITSHGELQYYL SLLNQQLPIESQMVSCLPDMNLAEIVLGNVQNA KDAVNWLGYAYLYIRMLRSPTLYGISHDDLKGD PLLDQRRDLVHTAALMLDKNNLVKYDKKTGN FQVTELGRIASHYYITNDTVQTYNQLLKPTLSEIE LFRVFSLSSEFKNITVREEKLELQKLLERVPIPVK ESIEEPSAKINVLLQAFISQLKLEGFALMADMVY VTQSAGRLMRAIFEIVLNRGWAQLTDKTLNLCK MIDKRMWQSMCPLRQFRKLPEEVVKKIEKKNFP FERLYDLNHNEIGELIRMPKMGKTIHKYVHLFPK LELSVHLQPITRSTLKVLTITPDFQWDEKVGSS EAFWILVEDVDSEVLHHEYFLKAKYAQDEHLI TFFVPVFEPLPPQYFIRVVS DRWLSCETQLPVSR HLILPEKYPPPTLDDLQPLPVSA LRNSAFESLYQ DKFPFFNPIQTQVFNTVYNSDDNVFVGAPTSGSK TICAFAILRMLLQNSEGRVCYITPMRLWQEQVY MDWYEFQDRLNKKVLLTGETSTDLKLLGKG NIIISTPEKWDILSRRWKQRKNVQNNLNFVVDV HLIGGENGPVLEVICSRRMYISSQIERPIRIVALSS LSNAKDVAHWLGCSATSTFNHPNVRPVPLELHI QGFNISHTQTRLLSMAKPVFHAITKHSPKPKVIVF VPSRKQTRLTAIDILTTCAADIQRQFLHCTEKDL IPYLEKLSDSLKETLLNGVGYLHEGLSPMERRL VEQLFSSGAIQVVASRSLCWGMNVAHLVHIM DTLYYNGKIHA YVDYPTIDVLQMVGHANRPLQ DDEGRVCVIMCQGSKKDFKKFLYEPLPVESHLD HCMHDHFNAEIVTKTIENKQDAVDYLTWTFLYR RMTQNPNNYNLQGISHRHLSDHLSSELVEQTLSDL EQSKCISIEDEMDVAPLNLGMIAAYYYINYTTIEL FSMSLNAKTKVRGLIETISNAEYENIPIRHHEDN LLRQLAQKVPKHLNPNPKFNDPHVKTNLLQLAHL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SRMQLSAELQSDTEEILSKAIRLIQACVDVLSSNG WLSPALAAMELAQMVTQAMWSEDSYLRRLPF PSGLFKRCTDKGVESVFDIMEMEDEERNALLQLT DSQIADVAFRCNRYPNIELSYEVVDKDSIRSGGP VVVLVQLEREEVETGPVIAPLFPQKREEGWVVV IGDAKSNSLISIKRLTLQKAKVKLDFVAPATGG RHNTLYFMSDAYMGCDQEYKFSVDVKEAETDS DSD
3620	A	1205	323	VIKMALAARLLPQFLHSRSLPCGAVRLRTPAVAE VRLPSATLCYFCRCRLGLGAALFPRSARALAASA LPAQGSRWVPLSSPGLPAAFASFPACQRSYSYE EKPQQHQKTKMIVLGFSPNPINWVRTRIKAFLIWA YFDKEFSITEFSEGAQAFHVSFKLLSQCKFDLL EELVAKEVLHALKEKVTSLPDNHKNALANDEI VFTSTGDISIYYDEKGRKFVNILMCFWYLTANIP SETLRGASVFQVKLGNNQNVETKQLLSASYEFQR EFTQGVKPDWTIARIEHKKLLE
3621	A	2	2995	SSSRSRHSSISPVRLPLNSSLGAELSRKKKRAAAA AAAAMDKGKESYERSGSGSYGRSPSPYGRRRSSS PFLSKRSLSRSPLSRKSMKSRSPAYSRHSSSH SKKKRSSSRSRHSSISPVRLPLNSSLGAELSRKKK ERAAAAAAAKMDGKESYERSGSGSYGRSPSPYG RRRSSPFLSKRSLSRSPLSRKSMKSRSPAYSRH SSSHSKKKRSSSRSRHSSISPVRLPLNSSLGAEL SRKKKRAAAAAAAAKMDGKESKSGSPVFLPRKE NSSVEAKDSGLESKLPKRSVKLEKSAAPDELNVN THLNTVEKNSSDTGKVKLDENSEKHLVKDLKAQ GTRDSKPIALKEEIVTPKETETSEKETPPPLTIASP PPPLPTTTPPPQTPPLPPLPIPALPQQPLPPSQPA FSQVPASSTSTLPPSTHSKTSVSSQANSQPPVQV SVKTQVSVTAAIHLKTSTLPPPLPPLPGDDDM DSPKETLPSKPVKKEKEQTRHLLTDLPLPELPG GDLSPDSPEPKAITPPQPPYKRPKICCPRYGER RQTESDWGKRCVDKFDIIGIIGEGTYGQVYKAKD KDTGELVALKKVRLDNEKEGFPITAREIKILRQ IHRSVVNMKEIVTDKQDALDFKKDKGAFYLVFE YMDHDLMLGLLESLVHFSEDHKSFMKQLMGL EYCHKKNFLHRDIKCSNILLNNSGQIKLADFGLA RLYNSEESRPYTNKVITLWYRPPKLLGEERYTP AIDVWSCGCILGELFTKKPIFQANLELAQLELISR LCGSPCPAVWPDVIKLPYFNTMKPKKQYRRRLR EEFSFIPSAALDLDHMLTLDPSKRCTAEQTLQSD FLKDVELSKMAPDLPWHQDCHELWSKKRRRQ RQSGVVVEPPPSKTSRKETTSGTSTEPVKNSSPA PPQPAPGKVESGAGDAIGLADITQQLNQSELAVL LNLLQSQTDLSPQMAQLNIHNSNPEMQQLEAL NQSISALTEATSQQQDSETMAPEESLKEAPSAPVI LPSAEQTTLEASSTPADMQNILAVLLSQLMKTQE PAGSLEENNSDKNSGPPQPRRTPTMPQEEAAGRS NGGNAL
3622	A	16	390	TPERGSAYPETAARRRPAGECPITMSDLEAKLST EHLGDKIKDEDIKLRVIGQDSSEIHFVKMTTPLK KLKKSQCQRQGVVNSLRFLFEGQRIADNHTPEE LGMEEDVIEVYQEIQIGHSTV
3623	A	2	1544	PPPAPGPDGLNEGCLHRLSMPHQRPRTCAMNPE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LTMESLGT LHGARGGGSGGGGGGGGGGGGGGGP GHEQELLASPSPHHARRGPRGSLRGPPTTAHQ ELGTAAAAAASRSAMVTSMASILDGGDYRPE LSIPLHHAMSMSCDSSPPGMGMSNTYTTLTPLQP LPPISTVSDKFHHPHPHHHPHHHHHHHQRLSGN VSGSFTLMRDERGLPAMNNLYSPYKEMPGMSQS LSPLAATPLGNGLGGLHNAQQSLPNYGPPGHDK MLSPNFDAAHTAMLTRGEQHLRGLGTPPAAM MSHLNGLHHPGHTQSHGVPVLAPSRERPPSSSSGS QVATSGQLEEINTKEVAQRITAELKRYSIPOAIFA QRVLCRSQGTLSDLLRNPKPWSKLKSGRETFRR MWKWLQEPEFQMSALRLAACKRKEQEPNKDR NNSQKKSRLVFTDLQRRTLFAIFKENKRPSKEMQ ITISQQLGLELTTVSNFFMNARRRSLEKWQDDLS TGGSSSTSSTCTKA
3624	A	27	2152	SARKAEAATSGTAARDGSGVGRNLVPPPSASAPK AEVESNEKDNRPEEEEQVIHEDDERPSEKNEFSR RKRSKSEMDMNVQSKRRRYMEEYEAEFQVKIT AKGDINQKLQKVIQWLLEEKLCALQCAVFDKTL AELKTRVEKIECNKRHKTVLTELQAKIARLTKRF EAAKEDLKKRHEHPPNPPVSPGKTVDVNSNN MSYRNAGTVRQMLSESKRNVSESAPPSFQTPVNT VSSNTLVTPPAVVSSQPKLQTPVTSGLTATSVLP APNTATVVATTQVPSGNPQPTISLQPLPVILHVPV AVSSQPQLQSHPGTLVTNQPSGNVEFISVQSPPT VSGLTKNPVSLPSLPNPTKPNNVSPVSPSIQRNP TASAAPLGTTLAVQAVPTAHSIVQATRTSLPTVG PSGLYSPSTNRGPIQMKIPISAFSTSSAAEQNSNT PRIENQTNKTIDASVSKKAADSTSQC GKATGSDS SGVIDLTMDDEESGASQDPKKNHTPVSTMSSSQ PVSRLQPIQPAPPLQPSGVPTSGPSQTTIHLPTA PTTVNVTHRPVTQVTRLVPVPRAPANHQVVYTT LPAPPAQAPLRGTMQAPAVRQVNPQNSVTVRV PQTTYVVNGLTLGSTGPQLTVHHRPPQVHTEP PRPVHPAPLPEAPQPQLPPEAGSTSRPSEATLEV SHA FRVKMAIVLVMECPGGGSKLCHC
3625	A	210	1115	ASPFLRPQGHDSGEREPFSQTPGLMQPFSIPVQIT LQGSRRRQGRATFPASGKKRETDYSDGDPLDVH KRLPSTGEDRAVMLGFAMMGFSVLMFFLLGTT ILKPFMLSQREESTCTAIHTDIMDDWLDCAFTCG VHCHGQGGKYPCLVFVNL SHPGQKALLHYNEE AVQINPKCFYTPKCHQDRNDLLNSALDIKEFFDH KNGTPFSCFYSPASQSEDVILIKKYDQMAIFHCLF WPSLTLLGGALIVGMVRLTQHL SLLCEKYSTVV RDEVGKVPYIEQHQFKLCIMRRSKGRAEKS
3626	A	9	921	SSVVEFSALSVSMACLSPSQLQKFQDGLVLEG FLSAEECVAMQQRIGEIVAEMDVPLHCRTEFSTQ EEEQLRAQGSTDYFLSSGDKIRFFFEKGVFDEKG NFLVPPEKSINKIGHALHAHDPVFKSITHSFKVQT LARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQD ASFLYTEPLGRVLGVWIAVEDATLENGCLWFIPG SHTSGVSRMRVAPVGSAPGTSFLGSEPARDNSL FVPTPVQRGALVLIHGEVVHKSQNLSDRSRQA YTFHLMASGTTWSPENWLQPTAELPFPQLYT
3627	A	231	644	INSSPRTGRDHQELNLHTERDSRSQRAVLKIPRQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				NPGIFYWIFLPSRSHSASHGSRQRQVSCQGTQDEI LKMRNTFAELKNSLEALSSRMDQAEERIGTQAG VQWRDHGSLQPQPPEFKQCFHLSLPSSWDYRAC LS
3628	A	2	810	GCKHLLQNSWYDPRVREADRVGQRARRPRAAM DWLMGKSKAKPNGKKPAAEERKAYLEPEHTKA RITDFQFKELVVLPREIDLNEWLASNTTTFHHIN LQYSTISEFCTGETCQTMAVCNTQYYWYDERGK KVKCTAPQYVDFVMSSVQKLVTDEDVFPTKYG REFPSSFESLVRKICRHLFHVLAHIYWAHFKETLA LELHGHNLNTLYVHFILFAREFNLLDPKETAIMDD LTEVLCSGGRRGSTVGA VGMGPAAGAPGAQNH VKER
3629	A	699	1604	CSHGSSAVSAWSPLFQASEVERQLSMQVHALRE DFREKNSSTNQHIIRLES LQAEIKMLSDRKRELEH RLSATLENDLLQGTVEELQDRVLILERQGHDKD LQLHQSQLELQEVRLSCRQLQVKVEELTEERSLQ SSAATSTSLSEIEQSMEAELEQEREQLTLLSVE MTALKEERDRLRVTSDEKPEQLQKAIRDRDE AIAKKNAVELELAKCRMDMMSLNSQLLDAIQQ KLNLSQQLEAWQDDMHRVIDRQLMDTHLKERS QPAAALCRGHSAGRGDEPSIAEGKRLFSFRKI
3630	A	423	1	PAKVLTLDIYLSKTEGAQVDEPVVITPRAEDCGD WDDMEKRSSGRRSGRRRGSQKSTDSPGADAELP ESAARDDAVFDDEVAPNAASDNASAEKKVKSPR AALDGGVASAASPESKPSPGTKGQLRGESDRSK QPPPASSP
3631	A	2082	674	WSGFWQLPGVRGVGSAPGGDGAFTSRRGSSRR PGAACPGCRGAGSERAPGGMGRRAPELYRAPF PLYALQVDPSTGLLIAAGGGGA AKTGKNGVHF LQLELINGRLSASLLHSHDTETRAMNLALAGDI LAAGQDAHCQLLRFQAHQQQGNKAEKAGSKEQ GPRQRKGAAPAEKKCGAETQHEGLELRVENLQA VQTDFFSDPLQKVVCFNHDNTLLATGGTDGYVR VWKVPSLEKVLFEKAHEGEIEDLALGPDGKLV VGRDLKASVWQKDQLVTQLHWQENGPTFSSTP YRYQACRFGQVPDQPAGLRLFTVQIPHKLRLRQP PCYLTAWDGSNFLPLRTKSCGHEVVSCLDVSES GTFLGLGTVTGSAIYIAFSLQCLYYVREAHGIV VTDVAFLPEKGRGPELLGSHETALFSVAVDSRCQ LHLLPSRRSVPVWLLLLLCVGLIIVTILLQSAFP FL
3632	A	942	40	PWCQRVEVRSCGSSKRSCSRWSGSSWDGSRSLG RGLNHTSLNRSPPFTPDMTMHCCSPCCQPTCCRT TCCRITTCWKPTTVTTCSSTPCCQPSCCVPSCCQ CCHPTCCQNTCCRTTCCQPTCVASCCQPSCCSTP CCQPTCCGSSCCGQTSCGSSCCQPICGSSCCQPC HPTCYQTICFRTTCCQPTCCQPTCCRNTSCQPTCC GSSCCQPCCHPTCCQTICRSTCCQPSCVTRCCSTP CCQPTCCGSSCCSQTCESSYCLPCCRPTCCQTT CYRTTCCRPSCCSPCCVSSCCQPSCC
3633	A	605	3004	GPEGYRGRRARHPSLGSTTGHC GGGRGAEGTGT DPAAPAARLNVDGLLVYFPYDYIYPEQFSYMRE LKRTLDAKGHVLEMPSGTGKTVSLLALIMAYQ RAYPLEVTKLIYCSRTPVPEIEKVIELRLKLLNFYE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KQEGEKLPFLGLALSSRNLCIHPEVTPLRFGKD VDGKCHSLTASYVRAQYQHDTSLPHCRFYEEFD AHGREVPLPAGIYNLDDLKALGRRQGWCPYFLA RYSILHANVVVYSYHYLLDPKIADLVSKELARK AVVVFDEAHNIDNVCIDMSVNLTRRTLDRCCQ NLETQKTVLRKETDEQRLRDEYRRLVEGLREA SAARETDAHLANPVLPEVLQEA VPGSIRTAEHF LGFLRRLLLEYVKWRLRVQHVVQESPPAFLSGLA QRVCIQRKPLRFCAERLSLLHTLEITDLADFSPL TLLANFATLVSTYAKGFTTHIEPFDDRTPTIANPIL HFSCMDASLAIKPVFERFQSVIITSGTSLSPLDIYPK ILDHFPVTMATFTMTLARVCLCPMIIGRGNDQVA ISSKFETREDIAVIRNYGNLLEMSAVVPDGVAF FTSYQYMESTVASWYEQGILENIQRNKLFIETQ DGAETSALEKYQEACENGRGAILLSVARGKVS EGIDFVHHYGRAVIMFGVPYVYTQSRLKARLEY LRDQFQIRENDFLTFDAMRHAAQCVGRAIRGKT DYGLMVFADKRFARGDKRGKLP RWIQEHLTDA NLNLTVDEGVQVAKYFLRQMAQPFHREDQLGL SLLSLEQLESEETLKRIEQIAQQL
3634	A	159	384	LKMSSKTASTNNIAQARRTVQQLREASIERIKV SKASADLMSYCEEHARS DPLLIGIPTSENPFKDKK TCIIL
3635	A	5	409	TELSQLEKAHPADMGRRKSKRKPPPKKKMTGT LETQFTCPFCNHEKSCDVKMDRARN TGVISCTV CLEEFQTPITCILGNLGGFFQRVGRGLESGPCSSGP L CALVQGQSRPEEQVPPSDFCGVRRCRAGFCQ
3636	A	48	282	DHLKSCYQDSHEDPTKMKRFLFLLLTISLLVMVQ IQTGLSGQNDTSQTSSPSASSMSGGIFLFFVANAI IHLFCFS
3637	A	1	1248	ARAGSVVGSAAARGPPAGCRCERAARLPSSPAR RRRCDWVEDGAGRMEILMTVSKFASICTMGAN ASALEKEIGPEQFPVNEHYFGLVNFNTCYCNSV LQALYFCRPFREKGLAYKSQPRKKESLLTCLADL FHSIATQKKKVGVI PPKKFITRLRKENELFDNYM QQDAHEFLNYLLNTIADILQEERKQEQNGRLPN GNIDNENNNSTPDPTVWHEIFQGTLTNETRCLTC ETISSKDEDFLDLSVDVEQNTSITHCLRGFSNTET LCSEYKYCEECRSKQEAHKRMKVKKLPMLAL HLKRFKYMDQLHRYTKLSYRVVFPLELRLFNST GDATNPDRMYDLVAVVVHCGSGPNRGHYIAIV KSHDFWLLFDDDDIVEKIDAQAIEEFYGLTSDISKN SESGYILFYQSRD
3638	A	11	630	PAGIPVSTISSDRRASTDLTRKMKPDETPMFDPNL LKEVDWSQNTATFSPAISPHTHPGGLVLRPLCTA DLNRGFFKVLGQLTETGVVSPEQFMKSFEHMKK SGDYVTVVEDVTLGQIVATATLIEHKFIHSCAK RGRVEDVVVSDECRGKQLGNLLSTLTLLSKKL NCYKITLECLPQNVGFYKKFGYTVSEENYMCRR FLK
3639	A	2	1200	PRVRLRPSRSRSCRGLLSTRAPGPSFRLHSSPL LPHAMKSPFYRCQNTTSVEKGNSAVMGGVLFST GLLGNLLALGLLARSGLGWCSRRPLRPLPSVY MLVCGLTVTDLLGKCLLSPVLAAYAQNRSRLRV LAPALDNSLCQAF AFMSFFGLSSTLQLLAMALE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				CWLSLGHPFFYRRHITLRLGALVAPVVSASFSLAF CALPFMGFGKFVQYCPGTWCFIQMVHEEGSLSV LGYSVLYSSLMALLVLATVLCNLGAMRNLYAM HRRLLQRHPRSCSTRDCAEPRADGREASPOPLEELD HLLLLALMTVLFTMCSLPVIYRAYYGAFKDVKE KNRTSEEADLRALRFLSVISIVDPWIFIIFRSPVFR IFFHKIFIRPLRYRSRCSNSTNMESSL
3640	A	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEY AIEAIKLGSTAIGIQTSEGVCLAVEKRITSPLMEPS SIEKIVEIDAHIGCAMSGLIADAKTLIDKARVETQ NHWFTYNETMTVESVTQAVSNLALQFGEEDADP GAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFV QCDARAIGSASEGAQSSLQEVYHKSMTLKEAICS SLILKQVMEEKLNATNIELATVQPGQNFHMF TK EELEEVIKDI
3641	A	2	1254	PTGQGGRRAEARSCLLSKAMLGRSGYRALPLGD FDRFQSSSFGFLGSQKGCLSPERGCVGTGADV PQ SWPSC LCHGLISFLGFLLLLVTFPISGW FALKIVPT YERMIVFRLGRJTPQGP GMVLLL PFIDSFORVDL RTRAFNVPPCKLASKDGA VLSVGADVQFRIWDP VLSVMTVKDLNTATRMTAQNAMTKALLKRPLR EIQMEK LKISDQLLEINDVTRAWGLEVD RVELA VEAVLQPPQDSPAGPNLDSTLQQLALHFLGGSM NSMAGGAPSPGPADTVEMVSEVEPPAPQVGARS SPKQPLAEGLLTALQPFLSEALVSQVGACYQFNV VLPSGTQSA YFLDLTTGRGRVGHGVPDGIPDVV VEMAEADLRALLCRELRPLGAYMSGRLKVKGD LAMAMKLEAVLRALK
3642	A	1	237	RRGEIDMATEGDVELELETETSGPERPPEKPRKH DSGAADLERVTDY AEEKEIQSSNLETAMSVIGDR RSREQKAKQER
3643	A	94	541	RKERRRRRRRMEAVVFVFSLLDCCALIFLSVYFII TLSDLECDYINARSCSKLNKWWIPELIGHTIVTV LLLSLHWFIFLLNLPVATWNIYRYIMVPSGNM GVFDPTEIHNRGQLKSHMKEAMIKLGFHLLCFF MYLYSMILALIND
3644	A	95	2808	TSCRHFPITSEDPLNYLLILTVERIYAYQALPLGFL FCSRDPVPEYLNHCGVKYVLISDRASFCAHIFFS PFRNVFRPAAGGGIAPPRLWFQPSLSDAEMEIPK LLPARGTLQGGGGGGIPAGGGRVHRGPDSPAGQ VPTRRLLLPRGPQDGGPGRRREEASTASRGPGPS LFAPRPHQPSGGGGGGGDDFFLVLLDPVGGDVE TAGSGQAAGPVLREEAEEGPGLOGGESGANPAG PTALGPRCLSAVPTPAPISAPGPAAAFAGTVTIHN QDLLLLRFENGVLTLATPPPHA WEPGAAPAQQPG CLIAPQAGFPAAHPGDCELPDLLLLAEPAEPAP APAPEEEAEGPAAALGPRGPLGSGPGVVLYLCPE ALCGQTFAKKHQLKMHLTHSSSQGQRPFKCPL GGCGWTF TTSYKLRHLQSHDKLRPFGCPAEGC GKSFTTVYNLKAHMKGHEQENSFKCEVCEESFP TQAKLGAHQ RSHFEPERPYQCAFSGCKKTFITVS ALFSHNRAHFREQELFSCSFPGCSKQYDKACRLK IHLRSHTGERPFLCDFDGC GWNFTSMKLLRHKR KHDDDRRFMC PVEGCGKSFTRAEHLKGHSITHL STKPFVCPVAGCCARFSARSSLYIHSKKHLQDQVD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TWKSRCPISSCNKLF TSKHSMKTHMVKRHKVGGQ DL LAQLEAANS LTPSSELT SQ RQNDLS DAEIVSLF SDVPDSTSAALLDTALVNSGILTIDVASVSSTLAG HLPANNNSVVGQAVDPPSLMATSDPPQSLDTSLF FGTAATGFQQSSLNMDEVSSVSVGPLGSLDSL MKNSSPEPQALTPSSKLTVDTIDTLTPSTLCE NSV SELLTPAKAEWSVHPNSDFFGQEGETQFGFPNAA GNHGSQKERNLITVTGSSFLV
3645	A	2194	1707	TVSFHKTMA SLK CSTVVCVICLEKPKYRCPACRV PYCSVVCFRKHKEQCNPETRPVEKKIRSALPTKT VKPVENKDDDDSIADFLNSDEEEDRVSLQNLKN LGESATLRSLLL NPHLRQLMVNLDQGEDKAKLM RAYMQEPLFVEFADCCLGIVEPSQNEES
3646	A	85	1948	ERGGGKAAAAAAAAAARALAAASGQDPRPHPR APPWDDSGDDDEATTPADKSELHHTLKNLSLKL DDLSTCNDLIAKHGAALQ RSL TELDGLKIPSESG EKLKVVNERATLFRITSNAMINACRDFLELAEIHS RKWQRALQYEQEQRVHLEETIEQLAKQHNSLER AFHSAPGRPANPSKSFIEGSL LTPKGEDSEEDDT EYFDAMEDSTSFITVITEAKEDSRKAEGSTGTSSA DWSSADNVLDGASLV PKGSSKVKRRVRIPNKNP YSLNLWSIMKNCIGRELSRIPMPVNFNEPLSMLQ RLTEDLEYHHLLDKA VHC TSSVEQMCLVAAF SV SSYSTTVHRIAKPFNPMLGETFELDRDDMGLRS LCEQVSHHPPSAAHYVFSKHGWSLWQEITISSKF RGKYISIMPLGAIHLEFQASGNHYVWRKSTSTVH NIIVGKLWIDQSGDIEIVNHKTNDRCQLKFLPYSY FSKEAARKVTGVVSDSQGKAHYVLSGSWDEQM ECKVMHSSPSSPSDGGKQKTVYQTL SAKLLWK KYPLPENAENMYFSELALTLNEHEEGVAPTDS RLRPDQRLMEKGRWDEANTEKQRLBEKQRLSR RRRLEACGPGSSCSSEE
3647	A	46	5007	PTGDACVSTSCELASALSHLDASHLTENLPKAAS ELGQQPMTELDSSSDLISSPGKKGA AHPDP SKTS VDTGQVSRPENPSQPASPRVTKCKARSPVRLPHE GSPSPGEKAAAPPDYSKTRSASETSPHNTRRV A ALRGAGPGAEGMTPAGAVLP GDPLTSQEQRQGA PGNHSALEMTGIHAPESSQEPSLLEGADSVSSR APQASLSMLPSTDNTKEACGHVSGHCCPGGSRE SPVTDIDSFikelDASAARSPSSQTGDSGSQEGSA QGHPPAGAGGGSSCRAEPVPGGQTSSPRRAWAA GAPAYPQWASQPSVLDSINPKHFTVNKNFLSN YSRNFSSFHEDSTLSGLGDSTEPSLSSMYGDAE DSSDPESL TEAPRASARDGWSPPRS RVSLHKED PSESEEEQIEICSTRGCPNPPSSPAHLPTQA AICPAS AKVLSLKYSTPRESVASPREKVACLP GSYSYTS GPD SSQPSSLLEMSSQEHEHADISTSQNHRPSCAEET TEVTSASSAMENSPLSKVARHFHSPPIILSSPNMV NGLEHDLDDDETLNQYETSINAAASLSSFSVDVP KNGESVLENLHISESQDLDDL LQPKMIARRPIM AWFKEINKHNQGT HLRSKTEKEQPLMPARSPDS KIQMVSSSQKKGVTVPHSPQPKNLENKDLSKK SPAEMLLTNGQKAKCGPKLRSLK GKAKVNSE APAANAVKAGGTDHRKPLISPQTSHKTL SKAVS QRLHVADHEDPDRNTTAAPRSPQCVLESKPPLAT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SGPLKPSVSDTSIRTFVSPLTSPKPVPEQGMWSRF HMAVLSEPDRCPTTPKSPKCRAEGRAPRADSG PVSPAASRNGMSVAGNRQSEPLASHVAADTAQ PRPTGEKGGNIMASDRLERTNQLKIVEISAEAVSE TVCGNKPAESDRRGGLAQGNCQEKSEIRLYRQ VAESSTSHPSLPSHASQAEQEMSRFSMAKLAS SSSSLQTAIRKAEYSQGGKSSLMDSRGVPRNSIPG GPSGEDHLYFTPRPATRTYSMPAQFSSHFGREGH PPHSLGRSRDSQVPVTSSVVPEAKASRGGLPSLA NGQGIYSVKPLLDTSRNLPADEGDIISVQETSCL VTDKIKVTRRHYCYEQNWPHESTSFFSVKQRIKS FENLANADRPVAKSGAPFLSVSSKPPIGRRSSGS IVSGSLGHPGDAAARLLRRSLSSCSENQSEAGTL LPQMAKSPSIMTLTISRQNPPESTSSKGSDELKKS LGPLGIPTPTMTLASPVKRNKSSVRHTQSPVSR KLQELRALSMPLDKLCESEDYSAGPSAVLFKTEL EITPRRSPGPPAGGVSCPEKGGNRACPGGSGPKT SAAETPSSASDTGEAAQDLFRRSWSVNLDQLLV SAGDQQRQLQSVLSSVGSKSTILTLIEAKAQSENE EDVCFIVLNRKEGSGLGFSVAGGTDVEPKSITVH RVFSQGAASQEGTMNRGDFLLSVNGASLAGLAH GNVLKVLHQAQLHKDALVVIKKGMDQPRPSAR QEPPTANGKGLLSRKTIPLEPGIGRSVAVHDALC VEVLKTSAGLGLSLDGGKSSVTGDGPLVIKRVY KGGAAEQAGIIEAGDEILAINGKPLVGLMHFDA WNIMKSVPEGPVQLLIRKHRNSS
3648	A	337	1564	KSRLSVTLMPVQLSEHPWNEISMHSRLRISVGGLP VLASMTKAADPRFRPRWKVVLTFFVGAAILWLL CSHRPAPGRPPTHNAHNWRLGOAPANWYNDTY PLSPPORTPAGIRYRIAVIADLDTESRAQEENTWF TYLKKGYLTFSDSGDKVAVEWDKDHGVLESHL AEKGRGMELSDLIVFNGKLYSVDDRTGVVYQIE GSAKVPWVILSDGDGTVEKGFKAEWLAVKDER LYVGGLGKEWTTTTGDVVNENPEWVKVVGK GSVDHENWVSNYNALRAAAGIQPPGYLIHESAC WSDTLQRWFFLPRRASQERYSEKDDERKGANLL LSASPDFGDIAVSHVGAVVPTHGFSSFKFIPNTDD QIIVALKSEEDSGRVASYIMAFTLDGRFLLPETKI GSVKYEGIEFI
3649	A	1	775	PTRPGSGSAGGARVGSGEFGVEMAALAPLPLPA QFKSIQHHLRTAQEHDKRDPVVAYYCRLYAMQ TGMKIDSKTPECRKFLSKLMDQLEALKQLGDN EAITQEI VGCAHLENYALKMFLYADNEDRAGR HKNMIKSFYTAALLIDVITVFGELTDENVKHKRY ARWKATYIHNCLKNGETPQAGPVGIEEDNDIEEN EDAGAASLPTQPTQSSSSTYDPSNMPSGNYTGI QIPPGAHAANTPAEVPHSTGVAK
3650	A	20	963	KMAATLGPLGSWQQWRRCLSARDGSRRLLLLL LLGSGQGPQQVGAGQTFEYLKREHLSKPYQGE APRPCFLRDWELQVHFKIHGQKKNLHGDGLAI WYTKDRMQPGPVFGNMDKFVGLGVFVDTPNE EKQQERVFPYISAMVNNGSLSYDHERDGRPTL GGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGK HEWRDCIEVPGVRLPRGYFGTSSITGDLSDNHD VISLKL FELTVERTPEEEKLHRDVF LPSVDNMKL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				PEMTAPLPPLSGLALFLIVFFSLVFSVFAIVIGIILY NKWQEQRKRKY
3651	A	1	1218	RSWAYVKKCKNNMCPNRLHDGPEPCWLHHA AGTVSAVQARGLQPSQSRSPRPVGLATALAYG PAHTPPLSRJGWAMQPPPGPLGDCLRDWEDLQ QDFQNIQVSAADAGSPPSRVSLAQGGSGSPGC KPSLPAAEAGAAQELNQMKERQGLFFDMEA YL PKKNGLYLSLVGNVNVTLSSKQAKFAYKDEYE KFKLYLTILILISFTCRFLNSRVTDAAFNLLVW YYCTLTIRESILINNGSRIKGWVVFHHYVSTFLSG VMLTWPDGLMYQKFRNQFLSFSMYQSFVQFLQ YYYQSGCLYRLRALGERHTMDLTVEGFQSWMW RVLTFLLPFLFFGHFWQLFNALTLFNLAQDPQCK EWQVLMCGFPFLLFLGNFFTLRVVHHKFHSQ RHGSKKD
3652	A	640	164	VTTSCIIPFAFGLGVRASERLAEIDMPYLLKYQPM MQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMG DRISMVQDPGSQAPTSWISQVFTTEVLTRI TELQRRFTWTPDQYLRGGLCAYSGGAGYVRSS QDLSCDFCNDVLARAKYLKRHGF
3653	A	2	909	IVRRDWQEVSDIHLAMANCKMTKSIRFPALEHC YTGGEVVLPKDQEEWKRRTGLLLYENYGQSETG LICATYWGMKIKPGFMGKATPPYDVQFHMEASV ENCHIVSMNTADPGSQGITHSLLQVIDDKGSILPP NTEGNIGIRIKPVRPVSFLMCYEGDPEKTAKVEC GDFYNTGDRGKMDEEGYICFLGRSDDIINASGYR IGPAEVESALVEHPA VAESA VVGSPDPIRGEVVK AFIVLTPQFLSHDKDQLTKELQQHVKSVTAPYKY PRKVEFVSELPKTITGKIERKELRKKETGQM
3654	A	2	909	IVRRDWQEVSDIHLAMANCKMTKSIRFPALEHC YTGGEVVLPKDQEEWKRRTGLLLYENYGQSETG LICATYWGMKIKPGFMGKATPPYDVQFHMEASV ENCHIVSMNTADPGSQGITHSLLQVIDDKGSILPP NTEGNIGIRIKPVRPVSFLMCYEGDPEKTAKVEC GDFYNTGDRGKMDEEGYICFLGRSDDIINASGYR IGPAEVESALVEHPA VAESA VVGSPDPIRGEVVK AFIVLTPQFLSHDKDQLTKELQQHVKSVTAPYKY PRKVEFVSELPKTITGKIERKELRKKETGQM
3655	A	2	2364	SPGPSLPESAESLDGSQEDKPRGSCAEPFTDTG MVAHINNSRLKAKGVGQHDNAQNFGNQSFEE RAACLRKGELFEDPLFPAEPSSLGFKDLGPN SKN VQNISWQRPKDII NNPLFIMDGISPTDICQGILGDC WLLAAIGSLTTCPKLLYRVVPRGQSFKKNYAGIF HFQIWQFGQWVNVVDDRLPTKNDKLVFVHST ERSEFWSALLEKAYAKLSGSYEALSGGSTMEGL EDFTGGVAQSFQLQRPQNLLRLLRKAVERSSL MGCSIEVTSDESLESM TDKMLVRGHAYSVTGLQ DVHYRGKMETLIRVRNPWGRIEWNGA WSDSAR EWEEVASDIQMQLLHKTEDGEFWM SYQDFLNN FTLLEICNLTPDTLSGDYKSYWHTTFYEGSWRTG SSAGGCRNHPGTFW TNPQFKISLPEGDDPEDDAE GNVVVCTCLVALMQKNWRHARQQGAQLQTIGF VLYAVPKEFQNIQDVHLKKEFFTKYQDHGFSEIF TNSREVSSQLRLPPGEYIIIPSTFEPHRDADFLLRV FTEKHSES WELDEVNYAEQLQEEKVSEDDMDQ

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DFLHLFKIVAGEGKEIGVYELQRLNRMIAIKFKS FKTKGFGLDACRCMNLMDKDGSGKLGLEFKI LWKKLKKWMDIFRECDQDHSGLNSYEMRLVIE KAGIKLNNKVMQVLVARYADDDLIDFDSFISCF LRLKTMFTFFLTMDPKNTGHICLSLEQVLGEGW EGICRIAPACPSTPPPPSSDVPGPASCPLFPWDL LPVSTVAADDHVGIEAL
3656	A	3	174	PLCTHYLLPELPEKSSRTSPRSRPGNMLSGDPHLP QPLCHCLDHCPCCFSGKRLVA
3657	A	1	444	DTRSTYHNAHSLPTYVKSPAPCQMTYIKSPAPCQ TQTCYVQGASPCQSYVQAPASGSTSQYCVTD CSAPCSTS YCC LAPRTFGVSPLRRWIQRPNQNT GSSGCCENSGSSGCCGSGGCGSCGCGSSGCCCL GIIPMKSRSPALL
3658	A	92	1537	SEAPVQPQPYTMTSFYSTSSCPLGCTMAPGARNV FVSPIDVGCQPVAEANAASMCLLANVAHANRVR VGSTPLGRPSLCLPPTSHTACPLPGTCHIPGNIGIC GAYGKNTLNGHEKETMKFLNDRLANYLEKVRQ LEQENAELETTLLERSKCHESTVCPDYQSYFRTIE ELQQKILCSKAENARLIVQIDNAKLAADDFRIKL ESERSLHQLVEADKCGTQKLLDDATLAKADLEA QQESLKEEQLSLKSNHEQEVKILRSQLGKFRIEL DIEPTIDLNRVLGEMRAQYEAMVETNHQDVEQ WFQAQSEGISLQAMSCSEELQCCQSEILELRCTV NALEVERQAQHTLKDCLQNSLCEADRYGTCLA QMQLSISNLEEQLSEIRADLERQNEQYQVLLDVK ARLENEIATYRNL TPLQSLFHACLLYFLSKLWPC HRWVSLWPWSQHGMILKARVRLRLVALGSG VPSPCPVFLQD
3659	A	2	402	DLLQCLNQLYASTEMSCQQSQQQCQPPPKCTP KCPPKCTPKCPPKCPPKQYAPCPPVSSCCG SSSGGCCSSEGGGCCLSHHRPRQSLRRRPQSSSC CGSGSGQQSGGSSCCHSSGGSGCCHSSGGCC
3660	A	26	710	CSAVEVKMAARTAFGAVCRRLWQGLGNFSVNT SKGNTAKNGGLLLSTNMKWVQFSNLHVDVPKD LTKPVVTISDEPDILYKRLSVLVKGHDKAVLDSY EYFAVLA AKELGISIKVHEPPRKIERFTLLQSVHI YKKHRVQYEMRTLRYRCLELEHLTGSTADVLEY IQRNLPQGVAMEVTKFCFFIFLDTIRTVTRTHQGA NLGNTIRRKRRKQVIKPQGGHFCLNLK
3661	A	2	370	DVSVAAASEPTVYRNPTKMSCQQNQQQCQPPPKC PIPKYPPKCPKSCASSCPPPISSCCGSSSGGCCSSG GCGCCSSEGGGCCLSHHRHHRSHCHRPKSSNCY GSGSGQQSGGSGCCSGGGCC
3662	A	205	1277	RKSLPHPNPQKMLKKPLSAVTWLCIFIVAFVSH AWLQKLSKHKTPAQPLKAANCCEEVKELKAQ VANLSSLLSELNKKQERDWWVVMQVMELESN SKRMESRLTDAESKYSEMNNQIDIMQLQAAQTV TQTSAGKETSPLRERGVPPLHQHCFYIPDDFLGS PELEVFCDMETSGGGWTIIQRRKSGLVSYFYRDW KQYKQGFSGIRGDFWLGNHHLRLSRQPTRLRVE MEDWEGNLRYA EYSHFVLGNELNSYRLFNGNY TGNVGN DALQYHNNTAFSTKDKDNDNCLDKCA QLRKGGY WYNCCTDSNLNGVYYRLGEHNKHL GITWYGWHGSTYSLKRVEMKIRPEDFKP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3663	A	64	1456	LSSAKETLAQMYNTVWNMEDLDLEYAKTDINC GTDLMFYIEMDPPALPPKPPKPTTVANNGMNNN MSLQDAEWYWGDISREEVNEKLRTADGTFLV RDASTKMHGDYTLTLRKGGNNKLIKIFHRDGKY GFSDDLTFSSVVELINHYRNESLAQYNPKLDVKL LYPVSKYQQDQVVKEDNIEAVGKKLHEYNTQFQ EKSREYDRLYEEYTRTSQEIQMKRTAIEAFNETIK IFEEQCQTQERYKEYIEKFKREGNEKEIQRIMHN YDKLSRRISEIISRRRLEEDLKKQAAEYREIDKR MNSIKPDLIQLRKTRDQYLMWL TQKGVRQKKL NEWLGNENTEDQYSLVEDDEDLPHHDEKTWNV GSSNRNKAENLLRGKRDGTFLVRESSKQGCYAC SVVVDGEVKHCVINKTATGYGFAEPYNLYSSLK ELVLHYQHTSLVQHNDNLNVTLAYPVAQQRR
3664	A	944	406	GATVEDQSCNFGSLRWVVSVPHISARSCDPLLS RTGRVPGGRGAGLPRHHSRCCCLQVFFNGANVR QVDVPTLTGAFGILAAHVPTLQVLRPGLVVVHA EDGTTSKYFVSSGSIAVNADSSVQLLAEAAVTLD MLDLGAANKLEKAQAEVGTADEATRAEIQIR IEANEALVKALE
3665	A	98	1388	ASQLAFGGKLTSTPSRDFQGCGRGAVTCCSFHEH RHQSGRCLSTGMAPNLKGRPRKKKPCPQRDSE SGVKDSNNNSDGKAVAKVKCEARSALT PKNN HNCKKVSNEEKPKVAIGEEGRADEQAFLVALYK YMKERKTPIERIPYLGFKQINLWTFQAAQKLG GYETITARRQWKHIYDELGGNPGSTSAATCTRR HYERLILPYERFIKGEEDKPLPIKPRKQENSSQE NENKTKVSGTKRIKHEIPKSKKEKENAPKQDAA EVSSEKEKEQETLISQKSIPEPLPAADMKKKIEGY QEFSAKPLASRVDPEKDNETDQGSNSEKVAEEA GEKGTPPLPSAPLAPEKDSALVPGASKQPLTSPS ALVDSKQESKLCCFTESPESEPQEASFRLPHHTG HRWQTRMRRRMTNCPWPQITLPTAP
3666	A	113	1492	LLQEMCTKTIPVLWGCFLNLVYSSSQTIYPGI KARITQRALDYGVQAGMKMIEQMLKEKKLPDL SGSELEFLKVDYVNYNFSNIKISAFSPNTSLAF VPGVGIKALTNHGATANISTDWGFESPLFVLYNSF AEPMEKPILKNLNEMLCPIHASEVKALNANLSTLE VLTKIDNYTLLDYSLISSPEITENYLDLNLKGIFY PLENLTDPPFSPVPFVLPERSNSMLYIGIAEYFFKS ASFAHFTAGVFNVTLSTEEISNHFVQNSQGLGNV LSRIAIEIYILSQPFMVRIMATEPPIINLQPGNFTLDI PASIMMLTQPKNSTVETIVSMDFVASTSVGLVIL GQRLVCSLSLNRFLALPESNRSNIEVLRFENILSS ILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEV LEGFLLISTDLKYETSSKQQPSFHVWEGNLISRQ WRGKSAP
3667	A	1	181	FRGRLGSGRNGGGS MNAPP AFESFLLFEGEKITIN KDTKVPNACLFTINKEDHTLGNIIK
3668	A	212	431	VAGEAVPFFPMYSEPLKPSYLALVLWYFLLTG YCITKPEVIFKIEQGEWPWILEKGFP SQCHPAKYL WCLHD
3669	A	458	1056	FSGVCFAGIAGSMATLLHDAVMNPAEVVKQRLQ MYNSQHRS AISCI RTVWRTEGLGAFYRSYTTQLT MNI PFQSIHFITYEFLQE QVNP HRTYNPQSHIISGG

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LAGALAAAATTPLDVCKTLTNTQENVALSLANIS GRLSGMANAFRTVYQLNLAGYFKGIQARVIYQ MPSTAISWSVYEFFKYFLTKRQLENRAPY
3670	A	145	298	RNPCPLTFLPSTLMVLLLSLTFFSALTFHSICQLRN TGVEVDIVFQRVSL
3671	A	3	462	ILKVAKKERTMSSLVPYKLPVSLSVGSCVHKGT PHSFINDPQLQVDFYTDMDSDIAFRFRVHFG NHVVMNRREFGIWMLEETTDYVPFEDGKQFELC IYVHYNEYEIKVNGHHLRALSHRIPPSFVEDGC KCPRRYLPWTSVCVCN
3672	A	1	1028	HYAKLGTRPRLKFMSSPSLSDLGKREPAADDE RGTQORRACANATWNSIHNGVIAVFQRKGLPDQ ELFSLNEGVRQLLKTSLGFFTEYLQNQLTKGM VILRDKIRFYEGQKLLDSLAEWDFSDVLPML QAIFYPVQGKEPSVRQLALLHFRNAITLSVKLED ALARAHARVPPAIVQMLLVLQGVHESRGVTEDY LRLETLVQKVVSPYLGTYGLHSSEGPFTHSILEK RLRRSRSGDVLAKNPVVRKSNTPLLPVQ HEAEGAAAGGTSIRRHVSSEMTSCPEPQGFSDPP GQPTGTFRSSPAPHSGPCPSRLYPTTQPPEQLD PTRS
3673	A	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYF TSSSVNSSAYTIYMGDKYENEDLIKHWPEDI WFHVDKLSSAHVYLRHLKGENIEDIPKEVLMD AHLVKANSIQGCKMNNVNVVYTPWSNLKKTAD MDVGQIGFHRQKDVKIVTVEKKVNEILNRLEKT KVERFPDLAAEKECRDREERNEKKAQIQEMKKR EKEEMKKKREMDELRSYSSLMKVENMSSNQDG NDSDEFM
3674	A	2	712	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYF TSSSVNSSAYTIYMGDKYENEDLIKHWPEDI WFHVDKLSSAHVYLRHLKGENIEDIPKEVLMD AHLVKANSIQGCKMNNVNVVYTPWSNLKKTAD MDVGQIGFHRQKDVKIVTVEKKVNEILNRLEKT KVERFPDLAAEKECRDREERNEKKAQIQEMKKR EKEEMKKKREMDELRSYSSLMKVENMSSNQDG NDSDEFM
3675	A	921	1321	VTAKMRVHISSCLKVQEQMANCPKFPVVPVPTS QIPSNIPNRSTFACPYCGARNLDQQLVKHCVE SHRSDPNRVVCPICAMPWGDPSYKSANFLQHL LHRHKFSYDTFVDYSIDEEAAFAALALSSEN
3676	A	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRR RRMISRYTRKAVPQSLELKGITKHALNHPPPEK LEEISPTSDSHEKDTSSQSKSDITRESSFTSADTGN SLSAFPSYTGAGISTEGSSDFSWGYGELDQNA KVQTMFTAIDELLYEQKLSVHTKSLQEECQQT ASFPHLRILGRQIITPSEGYRLYPRSPSAVSASYET TSLQERDSTIFGIRGKKLHFSSSYAHKASSIAKSSS FCSEMERDEEDSIIVSEGIIEEYLAFDHIDIEEGFHG KKSEAATEKQKLGYPPIAPFYCMKEDVLAYVFD SVWCKVVSCEQLTRSHWEGFASDDENAVT RPDSESSCVLSELHPLVLPVPQSKVLITSNPM LCQASRHQPNVNDLLVHGMPQLPRNLSLMDKLL DLDDKLLMRPGSSTILSTRNWPNAVEFSTSSLS YTVQSTRRRNPPRTLHPISTSHSACETPRSVEEIL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RGARVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVE HVSTVGPQRQMKPHGDSRAQSAVVDEPNYQQ PQERLLLPDFFPRPNTTQSFLDTQYRRSCAVEYP HQPARGRSAGPQLHGSTKSQSGRPVSRTRQG P
3677	A	246	757	MRLQGAIFVLLPHLGPILVWLFTRDHMSGWCEG PRMLSWCPFYKVLVVQTAIYSVVGYASYLVWK DLGGGLGWPLALPLGLYAVQLTISWTVLVFFT VHNPGALLHLLLYGLVVSTALIWHPIKLAAL LLPYLAWLTVTSALTYHLWRDSLCPVHQPOPT EKSD
3678	A	20	1508	RGKAEFFLAMAGTNALLMLENFIDGKFLPCSSYI DSYDPSTGEVYCRVPNSGKDEIEAAVKAAREAFP SWSSRSPQERSRVLNQVADLLEQSLEEFAQESK DQGKTLALARTMDIPRSVQNFRRFASSLHHTSE CTQMDHLGCMHYTVRAPVGVAGLISPWNPLPY LLTWKIAPAMAAGNTVIAKPSELTSVTAWMLCK LLDKAGVPPGVVNVFVGTGPRVGEALVSHPEVPL ISFTGSQPTAERITQLSAPHCKKLSLELGGKNPAII FEDANLDECIPATVRSSFANQGEICLCTSRIFVQK SIYSEFLKRFVEATRKWKVGIPSDPLVSIGALISK AHLEKVRSYVKRALAEGAQIWCGEVDKLSLPA RNQAGYFMLPTVITDIKDESCMTEEIFGPVTCV VPFDSEEEVIERANNVKYGLAATVWSSNVGRVH RVAKKLQSGLVWNTCNWLIRELNLPGGMKSSGI GREGAKDSYDFFTEIKTITVKH
3679	A	1862	502	MAGTKPYMEIQTIREYYEHL YANKLENLEEMD KFLDTYTLPRLNQEEVESLNRPTGSEIEAINSLP TKKIPGPDRFTAKFYQRYKEELSNLIHYLGLSHH LLALNFIIVSFGKKS AWSSAQVKVTDTFDGEV RVFEGPPKPEEPLKRSVVYIHGGGWALASAKIRY YDELCTAMAEELNAVIVSIEYRLVPKVYFPEQIH DVVRATKYFLKPEVLQKYMVDPRICISGDSAG GNLAAALGQQFTQDASLKNKLKQALIYPVLQA LDFNTPSYQQNVNTPILPRYVMVKYWVDYFKG NYDFVQAMIVNNHTSLDVEEAAAVRARLNWTS LLPASFTKNYKPVVQTTGNARIVQELPQLLDARS APLIADQAVLQLLPKTYILTCEHDVLRDDGIMYA KRLESAGVEVTLDFHEDGFHGCMTFSWPTNFSV GIRTRNSYIKWLDQNL
3680	A	249	2146	RSWGAPWFWRMRLRRRHMPRLAMVGCAFV LFLFLHRDVSSREEATEKPWLKSLVSRKDHVLD LMLEAMNNLRDSMPKLQIRAPEAQQTLSINQSC LPGFYTPAELKPFWERPPQDPNAPGADGKAFQK SKWTPLETQEEGYKKHCFNAFASDRISLQKSL GPDTRPPECVDQKFRRCPLATTSVIIVFHNEAWS TLLRTVYSVLHTTPAILLKEIILVDDASTEHLKE KLEQYVKQLQVVRVVRQEERKGLITARLLGASV AQAEVLTFDLAHCECFHGWLEPLLARIAEDKT VVSPDIVTIDLNTFEFAKPVQGRVHSGNFDWS LTFGWETLPPHEKQRRKDETYPIKSPTFAGGLFSI SKSYFEHIGTYDNQMEIWGGGENVEMSFVWQC GGQLEIIPCSVVGHVFRKSPHTFPKGTSVIARNQ VRLAEVWMDSYKKIFYRRNLQAAKMAQEKSF DISERLQLREQLHCHNFSWYLHNVPYEMFVPDL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TPTFYGAIKNLGTNQCLDVGENNRRGKPLIMYS CHGLGGNQYFEYTTQRDLRHNIKQLCLHVSKG ALGLGSCHFTGKNSQVPKDEEWELAQDQLIRNS GSGTCLTSQDKKPAMAPCNPSDPHQLWLFV
3681	A	2982	1869	LKDTLKSQMTQEASDEAEDMKEAMNRMIDEIN KQVSELSQLYKEAQAELEDYRKRKSLEDVTAEFY IHKAHEHEKLMQLTNVSRKAEDALSEMKSQYSK VLNELTQLKQLVDAQKENSVSITEHLQVITTLRT AAKEMEEKISNLKEHLASKEVEVAKLEKQLLEE KAAMTDAMVPRSSYEKLQSSLESEVSVLASKLK ESVKEKEKVHSEVVQIRSEVSQVKREKENIQTL KSKEQEVNELLQKFQQAQEELAEMKRYSESSSK LEEDKDKKINEMSKEVTKLKEALNSLSQSYS SSKRQSQQLEALQQQVKQLQNQLAECKKQHQE VISVYRMHLLYAVQGQMDDEDVQKVLKQILTMC KNQSQKK
3682	A	447	1024	AQALTAGRQLALAAPFIAPISPISLPRLNPPSQSW NSTPFFKVKLPPQKEVITSDELMAHLGNCLLSIKP QEKSEGLQLNFQQNVDDAMTVLPKLATGLDVN VRFTGVSDFEYTPECSVFDLLGIPLYHGWLVDPO QSPEAVRAVGKLSYNQL/VGEDHHLQTLQ*HQP RDRKPCRAVPGDHRGPSDLPRTV
3683	A	2	942	LEIKQEEKFVGQCIKEELMHGECVKEEKDFLKKE IVDDTKVKEEPPINHPVGCKRKLAMSRCTCGTE EAKYRCPRCMRYSCSLPCVKKHKAELTCNGVRD KTAYISIQQFTEMNLLSDYRFLEDVARTADHISR DAFLKRPISNKYMYFMKNRARRQGINKLLPNG FTKRKENSTFFDKKKQQFCWHVKLQFPQSQA\ST *KKRVPDDKTINEILKPYIDPEKSDPVIRQLKAYI RSQTGVQILMKIEYMQQNLVRYEYELDPYKSLLD NLRNKVIEYPTLHVVLKGSNNDMKVLHQVKSE STKNVGNEN
3684	A	119	1533	SLQENVQEKRVVCPGLGGLLPNGTPSITAAAAP QVLWRHVQPGCSHHLHACVIRAACRAGEGHAD RHAGPPET/PVTLPSWPWSSPWERQCPMHL*AP GHAFRPVPTTEHRRGWAALGHHRAAAGPLREPAS GSQPAPASC*PECHHGCEQTRQCQDLLREAVV APEQRG*PCHLQT*ATATLCPQVPAGRVWQP GHSCHLLPHRHDGSH*HHCAAHRRPVTRRQAAH GVPLPDACYSPHHTLPAAPPATRPAGHTATHPE *GGDLTPVPDGPDCPRDVQGIPAGGGSQALPC CPPFPAAPVSVQGTQGLGPKNVLH*QWEGIRWQ KEPE/PGPPPEVELKRGAKCRIGDHGLGAVLGQG EYAS*SPSIPW*ASSACPLHPTP/TVYTQSPAAA PGWTRPPSP/PPPGLYPGP/PASHAPGVRGGISHQL YSLP*LCRECCSCP/PPPPAHGGRCPSSLPEALAK LLL
3685	A	101	438	AWVLQCKINTELQTEVVMKSMVLWLGEQVQS LQLQQQLHCHFNNHTICVTNLEYNKEYPWDLV KAHLQGASTSNITFDIGELQKK\LDLKNQQTQEFQ PSL*AWTEFQQGLE
3686	A	105	845	VSDVVKNLVEVQCRQDGCDAVENVHQMFMF NWFTDCLWTLFLSNYQPSVESSSPGGSATSDDE FDPSADMLVHDFDDERTLEEEEMMEGETNFSSEI EDLAREGDMPIHELLSLYGYGSTVRLPEEDEEEE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EEEEGEDDEDADNDNSGCSGENKEENIKDSS GQDEETQSSNDPSQSVASQDAQEIRPRRCKYF DTNSEVEEESEDEDYIP/SIISFFQSSDGI*SSSSSE DWKKEIMVGS
3687	A	49	1225	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFN HTGELLATGDKGGRVVIFQREPESKNAPHSQGE YDVYSTFQSHEPEFDYLSLEIEEKINKIKWLPQQ NAAHSLSTNDKTIKLWKITERDKRPEGYNLKDE EGKLKDLSTVTSLQVPVLKPMDLMEVSPRRIFA NGHTYHINSISVNSDCETYMSADDLRINLWHLAI TDRSFTP/NIVDIKPANMEDLTEVITASEFHPHC NLFVYSSSKGSLRLCDMRAAALCDKHSKLFEEPE DPSNRSFFSEIS/SVSDVKFSHSDRYMLTRDYL VKVWDLNMEARPIETYQVHDYLRSKLCSLYEND CIFDKFECAWNGSDR/IIMTGAYNNFFRMFDRNT KRDVTLEASRGSSKPRAVL
3688	A	1	401	KKVPGRLSEMSFSLNFTLPANTTSSPVTDCGPSL GLAAGIPLL VATALLVALLFTLIHRRRSSIEAMEE SDRPCEISEIDNPKISENPRRSPTHEKNTMGAQE AHYVVKTVAGSEEPVHDYRPTIEMERRR
3689	A	698	889	GRVLVHCAMGVSRSATLVLAFLMIYENMTLVEA IPDGAGPPQISALTQAFVRQLQVLDNRLGRE
3690	A	61	153	MGAHLVRRYLGDASVEPDPLQMPTFFPDYGF
3691	A	61	153	MGAHLVRRYLGDASVEPDPLQMPTFFPDYGF
3692	A	3	2831	PLVRRLLRQTLRRVGGARAVREAVMRAVL TWR DKAEHCINDIAFKPDGTQLILAAGSRLLVYDTS GTLLQPLKGHKDTVYCVAYAKDGKRFASGSAD KSVIWT SKLEGILKYTHNDAIQCVSYNPITHQLA SCSSSDFGLWSPEQKSVSKHKSSSKIICCSWTNDG QYLALGMFNGIISIRNKNKEEKVKIERPGGSLSPI WSICWNPSSRWESFWMNRENEDAEDVIVNRYIQ EIPSTLKSAVYSSQGSEAESEEEPEEDDSPRDDNL EERNDILAVADWG/QKVSFYQLSGKQIGKDRAL NFDPCISYFTKGEYILLGGSDKQVSLFTKDGVR LGTVGEQNSWVWTGQAKPDSNYVVGCGQDGTI SFYQLIFSTVHGLYKDRYAYRDSMTDVIVQHLIT EQKVRIKCKELVKKIATYRNRLAIQLPEKILYELY SEDLSDMHYRVKEKIIKKFECNLLVVCANHILC QEKRLQCLSFSGVKEREWQMESLIRYIKVIGGPP GREGLLVGLKNGQLKIFVDNLFAIVLLKQATAV RCLDMSASRKKLA VVDENDTCLVYDIDTKELLF QEPNANSVAWNTQCEDMLCFSGGGYLNIAKSTF PVHRQKLQGFVVGYNGSKIFCLHVFSISAVEVPQ SAPMYQYLDRLKFKEAYQIACLGVTDTDWRELA MEALEGLDFETAKKERKKRGETNNDLFLADVFS YQKGFHEAAKLYKRSGHENLALEMYTDLCMFE YAKDFLGS GPKETKMLITKQADWARNIKEPKA AVEMYISAGEHVKAIEICGDHGWVDM LIDIARK LDKAEREPLLLCATYLLKKLDSPGYAAETYLKMG DLKSLVQLHVETQRWDEAFALGEKHPEFKDDIY MPYAQWLAENDRFEEAQKAFHKAGRQREAVQV LEQLTNNAVAESRFNDAAYYYWMLSMQCLDIA QDPAQKD
3693	A	3	1099	SSFTCMRTVFHSNTSVSSLLHRPGHVTPQLTIHG GWRHHRDHTAIDEWDFNPSKFLIYTCLLLFSVLL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				PLRLDGIIQWSYWAVFAPILWLKLLVVGASVAGVWARNPRYRTEGEACVEFKAMLIAGVGHLLLMFEVLVCDRVERGTHFWLLVFMPFFVSPVSAACVWGRHRSLELEILCSVNILQFIFALKLDRIHWPWL VVFVPLWILMSFCLVVLYYIVWSLLFLRSLDVVAEQRRTHVTMAISWITVPLLTTFEVLLVHRLDGHNTFSYVSIFVPLWLSLLTLMATTFRRKGGNHWWFAIRRD/CQDQLPQPTGKPPPPPLTDH HGEKALPLQNKDRGSPASRGSPRL
3694	A	483	761	PRSLIDYKSYM DTKLLVARFLEQSSCTMTDPDIHE LVENIKSVLKSDEEHMEEAITSASFLEQIMAH SXQHRAHKLPXETAGLXTSELRLXLP
3695	A	483	761	PRSLIDYKSYM DTKLLVARFLEQSSCTMTDPDIHE LVENIKSVLKSDEEHMEEAITSASFLEQIMAH SXQHRAHKLPXETAGLXTSELRLXLP
3696	A	456	733	L SAALWEEPILSLWSETKELTNRGKMNY PQIGPH RPHVKGLRVRPGPTLSNAPKSLCPGMSNSDRGI HGGEGQGPGKRAGHLGRGGGMSFL
3697	A	877	1873	VWL*TLS*HTCALMTVCRSCLVKYLEENNTCPT CRIVHQSHPLQYIGHDRMQDIVYKLV PGLQEA EMRKQREFYHKLGMVPGDIKGETCSAKQHLDS HRNGETKADDSNKEAAE
3698	A	1	572	KQCGIPHEVVRDENSSVYAEVSRLLLATGHWKR LRRDNPRFNLMLGERNRPFGR LGHEPGLVQLV NYR GADKLCRKASLVKLIKTSPELAESCTWFPE SYVIYPTNLKTPVAPAQNGIQPPISNSRTDEREFFL ASYNRKKEDGEGNVWIAKSSAGAKVWVQW*M TDLEEDIPSPVGLGLESEWPL
3699	A	2008	2432	LHCKMGALETQTHPCSQNMLRSLQKCCCKVEE HHLQPVQVLQTL LHSATAGTGCRRPAPPPAPPT PTPWRSRQSGKQSERAS*LKGRGRYGLGALGGR GGRALGGSRWPPPLPGETLFSGCKHRRRRRGSD AAPGEEAGT
3700	A	33	1318	GYQIGMALASGPARRALAGSGQLGLGGFGAPRR GAYEWGVRSTRKSEPPPLDRVYEIPGLEPITFAG KMHFVPWLARPIFPWDRGYKDPRFYRSPPLHE HPLYKDQACYIFHRCRLLEGVKQALWLT KTKL IEGLPEKVLSLVDDPRNHENQDECVLNVISHARL WQTTEEIPKRETYCPVVDNLIQLCKSQILKHPSL ARRVCVQNSTFSA TWNRESLLQVRGSGGARLST KDPLPTIASREEIEATKNHVLET FYPIPIIDLHECN IYDVKNDTGFQEGYPYPHTLYLLDKANLRPH RLQPDQLRAKMILFAFGSALA QARLLYGNDKAV LEQPVVVQSVGTDGRVFHFLVFQLNTTDLDSNE GVKNLA WVDSDQLLYQHFWCLPVIKRRVVVEP VGPVGFKPETFRKFLALYLHGAA
3701	A	86	465	WTL CGPEAGMVGYPKPDGRNNTKFQVAVAGS VSGLVTRALISPF DVIKIRFQLQHERLSRSDPSAK YHGILQASRQILQEEGPTAFWKGHVPAQILSIGY GAVQFLSFEMLT ELVHRGSVVDARE
3702	A	166	814	GFWEKTNQSSHSMDPLGAPSQFVDVDTLPSWGD SCQDELNSSDTTAEIFQEDTVRSPFLYNKD VNGK VVLWKGDVALLNCTAIVNTS NESLTDKNPVSESI FMLAGPDLKEDLQKLKG CRTGEAQLTKGFNLAA RFIHTVGPKYKSRYRTAAESSLYSCYRNVQLA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KEQSMSSVGFCVINS AKRGYPLK DATHIALR TVR RFLEIHGETIEKVV
3703	A	128	1255	SLGPSK SATIPCCGDTMAPEEDAGGEALGGSFW EAGNYRRTVQRVEDGHR LCGDLVSCFQERARIE KAYAQQ LADWARKWRGTVEKG PQYGTLEKAW HAFFTA AERLSALHLEVREKLQGDSEVR A WQ RGAFHRPVLGGFRESRAAEDGFRKAQKPWLKRL KEVEASKKSYHAARKDEKTAQTRESHAKADSA VSQEQLRKLQERVERCAKEAEKTKAQYEQTLAE LHRYTPRYMEDMEQAFETCQAAERQRLFFKD MLLTLHQHLDLSSSEKFHELHRDLHQGIEAASDE EDLRWWRSTHGPGMAMNWPQFEESLD TQRTI SRKEKGG RSPDEVTLTSIVPTRDGTAPPPQSPGSP GTGQDEEWSDEESP
3704	A	1	271	ARGEDLALATGGGPD TVTHSNMPCPN SLVYDC WLNIECSVGEHTFEDLGLCPGRNQREKKRSYK DFLREEEKIAAQVRNSSKKLKDSE
3705	A	170	1318	LNWANLVIMWPREEEKEKVQDYSLGGLSPDLRI DVSRRKKILKAYDEDEDEDLYPDHPPPSLPLPG QFTCPQCRKSFTRRSFRPNLQLANMVQIIRQMCP TPYRGNRNDQGMCFKHQEALKLCEVDKEAIC VVCRESRSHKQHSVLPLEEVVQEYKAKLQGHVE PLRKHLEAVQKMKAKEERRVTELKSQMKSELA AVASEFGRLTRFLAEEQAGLERRLREMHEAQLG RAGAAASRLAEQAAQLSRL LAEAQERSQQGGIR LLQDIKETFNRC EEVQLQPPEVWSPDPCQPHSHD FLTDAIVRKMSRMFCQAARVDLTLDPDTAHPAL MLSPDRRGVRLAERRQEVADHPKRFSADCCVLG AQGFRSGRHYWEVCMGP
3706	A	204	1996	SRERQTTWMDHNFAPAPPEMQSHGAPGPGTSFS HSHVLGRPIRPSRLPGGGSPLTPVLRKTIHLDTFP QSHIPQTSSRLGLGARTRSVPQETGIALGASLSP LPTSSLVPRKLSSISLTLHQNSQARSLDRPLSHWE ELPTPGKKAAPHEGGRVSSPGSPVTLVPGGRVH SEGPGNPGLTKSNRMLATEKPLVSSYLALPFQSR LAQSAPVLAEPGSLGQGHLSVTDHMPTRA SPG KKGPRARGIPRPRGRLQRANTTVNLTAMDTRTD AARHLATMATNRPSLAINLATPNTSQLDTGTEFP ALDIKLTARDLSSVGT VKSGKTVNLATAGTIKP GTAMNLT TVGTTKPGMVMDLIASEPDKLGKAM ATRSTAKPDMTTEGIAMDSATSDPVKPDITATV GTSRLETAMALARVNRAKLTAKNSLALDTSR MGTAVGSVVPVTPDPATGKTTLGSVNNLTISDV ATCLLMPSRSTDLALDNTNAAMDRA TEPA SLDL ATEYK GKCRNLVGDGLGREGEVCELGDGSMK PMSINSNLLGYIGIDTIEQMRKKTMTGTFDFNIM VVGTEGCGAAAGLVAGSTKDPISFPQ
3707	A	3	549	SSSISRDFLGQAACASGTMLRWLRDFVLPTAACQ DAEQPMRYETLFQALDRNGDGVVDIGELQEGLR NLGIPLGQDAEEKIFTTGDVNKDGKLD FEEFMKY LKDHEKKMKLAFKSLDKNNDGKIEASEIVQSLQ TLGLTISEQQAELILQSIDVDGTMTVDWNEWRD YFLFNPVTDIEEIR
3708	A	1	1866	EFRGAGRANMLAPRGAAVLLHLVLQRWLAAG AQATPQVFDLLPSSSQRLNPGALLPVL TDPALND

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LYVISTFKLQTKSSATIFGLYSSTDNSKYFEFTVM GRLSKAILRYLKNDBGK VHLVVFNNLQLADGRRH RILLRLSNLQRGAGSLELYLDCIQVDSVHNLPR FAGPSQKQPETIELRTFQRKPQDFLEELKL VVRGSL FQVASLQDCFLQQSEPLAATGTGDFNRQFLGQM TQLNQLLGEVKDLLRQEVNETSFLRNTITECQAC GPLKFQSPSTPSTVPPASPAPTRPPRCDSNPCF RGVQCTDSRDGFQCGPCPEGYTGNITCIDVDEC KYHPCYPGEHCINLSPGFRCDACPVGFTGPMVQ GVGISFAKSNKQVCTDIDECRNGACVPNSICVNT LGSYRCGPCKPGYTGDIQIRGCKAERNCRNPELN PCSVNAQCIERQGDVTCVCGVGWAGDGYICGK DVDIDSYDEELPCSARNCKKDNCKYVPNSGQE DADRDGIGDACDEADGDGILNEQDNCVLHNV DQRNSDKDIFGDACDNCNLSVLNNDQKDTDGDG RGDACDDMDGDGIKNILDNCPKFPNRDQRDK DGDGVGDACDSCPDVSNPNQ
3709	A	144	417	TQAMEGLLHYNPAHAISLLSALNEERLKGQLCD VLLIVGDQKFRAHKNVLAASSEYFQSLFTNKENE SQTVMFLDFCEPDADFNVNLNYIY
3710	A	245	688	FGMLKNKGHSSKKDNLAVNAVALQDHILHDLQ LRNLSVADHSKTQVQKKENKSLKRDTKAIDTGL KKTTCQPKLEDSEKEYVLDPKPPPLTLAQKLGLI GPPPPPLSSDEWEKVKQRSLLQGDSVQPCPICKE EFELRPQVFSIRG
3711	A	3	773	SLEMSSDGEPLSRMDSSEDSISSTIMDV DSTISSGRS TPAMMNGQGSTTSSSKNIAYNCCWDQCQACFNS SPDLADHIRSIHVDGQRGGVFVCLWKGCKVYNT PSTSQSWLQRHMLTHSGDKPFKCVVGGCNASFA SQGGLARHVPHTFSQQNSSKVSSQPKAKEESPSK AGMNKRRKLKNKRRRSLARPHDFFDAQTLDAIR HRAICFNLSAHIESLGKGHSVVFHSTVSILLFFQIK YKTLQKNISTIHSKSLKI
3712	A	2	344	RATWHNAGKEREAVQLMAGAEKRVKASHSFLR GLFGGNTRJEEACEMYTRAANMFKMAKNWSAA GNAFCQAALHMQQLQSKHDSATSFVDAGNAYK KADPQGKTARHVACYLCV
3713	A	20	974	GAAATACSSSSSSSGAPATWAAHGPBKDVASPS SVSLSPRRSRLVLRCGLRRNPERPSSSPALRRL LLLLLLLLLLGFLSPGPERGVGGGRFGRRAL LWAAALGHVVSGKVMSSRAPGSRLSSGGGGGG TNYSRSWNDWQPRDTSASADPGNLKYSSSRDRG GSSSYGLQPSNSAVVSRQRHDDTRVHADIQND KGGYSVNGSGENTYGRKSLGQELRVNNVTSPE FTSVQHGSRALATKDMRKSQERSMSYCDERLS YLLRRITRENDRRLATVKQLKEFIQQPENKLV LVKQLDILAAVHVDLNER
3714	A	237	458	IFALKSPSYLLPCCTPEGKMDHKQLCWSPQKSG QSSRSCCICSNQHGLIWKYSNLMCLQCCHQYVK DIGFIKL
3715	A	970	1524	LCTLSPGISGTAGSCLTTEPGTELGTSAQNGFYH EAVVLTQALKLNPQDHRLFGNRSFCHERLGQP AWALADAQVALTLRPGWPRGLFRLGKALMGLQ RFREAAAVFQETLRGGSQPDAAARELRSCLLHLTL QGQRGGICAPPLSPGALQPLPHAEAPSGPLSLRC

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				PRSTALRSPGLSPLLH
3716	A	85	308	QGLPSTMVKLGCSFSGKPGKDPGDQDGAAMDS VPLISPLDISQLQPPLPDQVVIKTQTEYQLSSPDQQ NYTKSR
3717	A	58	618	GAGCTSPGLWARKAAARCLFTYPSRAQPSNVGR RRRRRPGLGALAAGVPAMAESVERLQQRVQELE RELAQERSLQVPRSGDGGGGRVRIEKMSSEVVD SNPYSRLMALKRMGIVSDYEKIRTFVAIVGVGG VGSVTAEMLTRCGIGKLLLFDDYDKVELANMNR LFFQPHQAGLSKVQAAGHTPEE
3718	A	3	593	RGAGGRAGGRADGQPNMADQRQSLSTSGESL YHVLGLDKNATSDDIKKSRYKLALKYHPDKNPD NPEAADKFKEINNAHAILTDATKRNIYDKYGSGL LYVAEQFGEENVNTYFVLSSWWAKALFVFCGLL TCCYCCCCCCCCFNCCKGCKPKAPEGEETEFY VSPEDLEAQLQSDEREATDTPIVIQPASATEP
3719	A	2	2173	SGGVRMGSRADGPRTSGHVTGKMAVFPWHSRN RNYKAEFASCRLEAVPLEFGDYHPLKPITVTESK TKKVNRRKGSTSSSSSSSVVDPLSSVLDGTDPL SMFAATADPAALAAAMDSSRRKRDRDDNSVVG SDFEPWTNKRGEILARYTTTEKLSINLFMGSEK KAGTATLAMSEKVRTRLEELDDFEESQKELLN LTQQDYVNRIBELNQLKDAWASDQKVKAAPKN VHPGKLVYERIFSMCVDSRSVLPDHFSPENANDT AKETCLNWFFKIASIRELIPRFYVEASILKCNKFLS KTGISECLPRLTCMIRGIGDPLAGSVYARAYLSRV GMEVAPHLKETLNKNFFDFLLTFKQIHGDTVQN QLVVQGVELPSYLPYPPAMDWIFQCISYHAPEA LLTEMERCKKLGNALLNSVMSAFRAEFAT RSMDFIGMIKECDESGFPKHLLFRSLGLNLALAD PPESDRLQILNEAWKVITKLKNPQDYINCAEVWV EYTCKHFTKRENTVLADVHKHMTDPRAFEDSY PQLQLIKKVIAHFHDFSVLFSVEKFLPFLDMFQK ESVRVEVCKCARTPLSSINKSPRTRSS*MPFCMF ARPCMTL/CNALTLEDEKRMLSYLINGFIKMOVSF GRDFEQQLSFYVESRSMFCNLEPVLVQLHSVNR LAMETRKVMKGNHSRKTA AFVRSWGAYWFITIP SLAGIFTRLNLYLHSG
3720	A	24	296	ENLFRAGFAFSLRSSFYISKTYCSWFNLSIGSL ADFNKSGTRDYSRQMAVRE/KVFDVIRCFKRH GAEVIDTPVFELKVRNGQEETW
3721	A	2	310	PSCLTCVGHCSIGGSCTMIGIMPECHCSLHMTG PRCEEHVFIQQPGHIASILPLLVLALLALVAGVV FWHKRRVQGAKGFGHQHRTNGAMNVEIGNPTY K
3722	A	75	722	MELVAGCYEQVLFGFAVHPEPEACGDHEQWTL VADFTHHHAHTASLSAVAVNSRFVVTGSKDETHI YDMKKKIEHGALVHSGTITCLKFYGNRHLISGA EDGLICIWDAKKWECLKSIKAHKQVTFLSIHPS GKLALSVGTDKTLRTWNLVEGRSAFIKNIKQNA HIVEWSPRGEQYVVIQNKIDIYQLDTASISGTITN EKRISSVKFLSES
3723	A	110	316	MELSDNRRSGGLEGLAEKCPNLTYNLNLSGNKIK DLSTVEALVSGTVLSLDLLFLVKFSEICLLISI
3724	A	3	406	VDRGTEAWQRDPAFSGLQRVGGVDVSFVKGDS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VRACASLGVLSPFELEVVEESRMVSLTAPYVSG FLAFREVPFLLLVQQLREKEPGLMPQVLLVDGN GVLHHRGFGVACHLGVLTDLPCVGVAKKLLQV DG
3725	A	3	406	VDRGTEAWQRDPFSGLRVGGVDVSVFKGDS VRACASLGVLSPFELEVVEESRMVSLTAPYVSG FLAFREVPFLLLVQQLREKEPGLMPQVLLVDGN GVLHHRGFGVACHLGVLTDLPCVGVAKKLLQV DG
3726	A	1	433	SSDDRSLEFRRLKLNIAIFDEGHMLKNMGSIYQ HLMNTINANNRLLL TGTVPQNNLELMSLLNFVM PHMFSSSTSEIRRMFSSSKTKSADEQSIYEKERIAH AKQIIKPFILRRVKEEV LKQLPPKKDRIELCAMSE KQEQLYLG
3727	A	6	383	RIPRGKACXTVLGRSTGELEGFASSRLPPQPCGW GQSSDLLSRIDLDELMMKDEPPLDFPD TLEGFEY AFNEKGQLRHIKTGEFVFNYREHLHRWNQKRY EALGEITKYVYELLEKDCNSKKVS
3728	A	3	2452	EIAGAAAENMLGSLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQELESCSG LGSTSDDDTDVREVSSRPSTPGLSVVSGISATSE DIPNKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLY LQPKQHFQHIEAEADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAFKQ RHS/YTPERLVRSSSDIVSSVRRPMSDPSWNR RPGNEERELPPAAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDEKSDRNRPWWRKRFVSAMPK APIPFRKKEKQEKDKDDLGPDRFSTLTDDPSR LSAQAQVAEDILDKYRNAIKRTSPSDGAMANYEST EVMGDGESAHDSRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKLRLALCSADSVAFVLT HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLRVLR DKEVANRYFTTVCVRLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVV TANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTAA VEFIKTIDD RK
3729	A	3	2452	EIAGAAAENMLGSLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQELESCSG LGSTSDDDTDVREVSSRPSTPGLSVVSGISATSE DIPNKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLY LQPKQHFQHIEAEADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHEGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAFKQ RHS/YTPERLVRSSSDIVSSVRRPMSDPSWNR RPGNEERELPPAAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDEKSDRNRPWWRKRFVSAMPK APIPFRKKEKQEKDKDDLGPDRFSTLTDDPSR LSAQAQVAEDILDKYRNAIKRTSPSDGAMANYEST

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EVMGDGESAHDSRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKKLRLALCSADSVAFPVLT HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRLKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLQRVLR DKEVANRYFTTVCVRLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFVLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTA AVEFIKTIDD RK
3730	A	3	2452	EIAGAAAENMLGSLCLPGSGSVLLDPCTGSTISE TTSEAWSVEVLPSDSEAPDLKQEERLQLESCSG LGSTSDDTDVREVSSRPSTPGLSVVSGISATSEDP NKIEDLRSECSSDFGGKDSVTSPDMDEITHDFLYI LQPKQHFQHIIEAADMRIQLSSSAHQLTSPPSQSE SLLAMFDPLSSHGASAVVRPKVHYARPSHPPPD PPILEGAVGGNEARLPNFGSPMF*LPAEMEAQKQ RHS/YTPERLVRSSSDIVSSVRRPMSDPSWNR PGNEERELPPAAIGATSLVAAPHSSSSSPSKDSS RGETEERKDSDEKSDRNRPWWRKRFVSAMPK APIPFRKKKEKQEKDKDDLGPDRFSTLTDDPSRPLS AQAQVAEDILDKYRNAIKRTSPSDGAMANYEST EVMGDGESAHDSRDEALQNISADDLPDSASQA AHPQDSAFSYRDAKKKLRLALCSADSVAFPVLT HSTRNGLPDHTDPEDNEIVCFLKVQIAEAINLQD KNLMAQLQETMRCVCRFDNRTCRLKLLASIAEDY RKRAPYIAYLTRCRQGLQTTQAHLERLLQRVLR DKEVANRYFTTVCVRLLESKEKKIREFIQDFQK LTAADDKTAQVEDFLQFLYGAMAQDVIWQNAS EEQLQDAQLAIERSVMNRIFKLAFYPNQDGDILR DQVLHEHIQRLSKVVTANHRALQIPEVYLREAP WPSAQSEIRTISAYKTPRDKVQCILRMCSTIMNLL SLANEDSVPGADDFVPVLVFVLIKANPPCLLSTV QYISSFYASCLSGEESYWWMQFTA AVEFIKTIDD RK
3731	A	1	1305	VNTAMHEAKLMEECDELVEHQQRKQMIQIAVKIK ETKVMKLRKLAQQVANCRCCLERSTVLINQAEH ILKENDQARFLQSAKNIAERVAMATASSQVLIPDI NFNDAFENFALDFSREKKLLEGLDYLTA PNPPSIR EELCTASHDTITVHWISDDEFSISSYELQYTIFTGQ ANFISLYNSVDSWMIVPNIKQNHYT VHG LQSGTR YIFIVKAINQAGSRNSEPTRLKTN SQPFKLPKMT HKKLKISNDGLQMEKDESSLKKSHTPERFSGTGC YVYGV LHNSDNS*MFISLSFPLSHRYAIGIAYKSA PKNEWIGKNASSWVFSRCNSNFVVRHNNKEML VDVPPHLKRLGVLLDYDNY/NMLSFYDPANSLAH LHTFDVTFILPVCPTFTIWNKSLMLSGLPAPDFI DYPERQECNCRPQESPYVSGMKTCH
3732	A	127	2832	LGQRLSLVPRPSLKRRLGKRLSLGLRERMMSLW WS/GPKVRTQATTGARPKTETKSVPAARPKTEAQ AMSGARPKTEVQVMGGARPKTEAQGITGARPKT DARAVGGARSKTDAKAIPGARPKDEAQA WAQS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EFGTEAVSQAEGVSQTNAVAWPLATAESGSVTK SK\ACLWIEN*SMWM/PETFPQTGGQKGIQPWFG PGEETNMGSWCYSRPRAREEASNESGFWSADET STASSFWTGEETSVRSWPREESNTRSRRHAKHQT NPRSRRPRSKQEAYVDSWSGSEDEASNPF5FWVG ENTNNLFRPRVREEANIRSKLRTNREDCFESESED EFYKQSWVLPGEEAN\IDSGTETKKILLPWKLRA QKDVDSDRVKQEPFEEVIGSWFWAEKEASLE GGASAICESEPGTEEGAIGGSAYWAEKSSLGAV AREEAKPESEEEAIFGSWFWRDEACFDLNPCPV YKVSDFRDAAEELNASSRPQTWDEVTVFEKPG LFHGVGFRSTSPFGIPEEASEMLEAKPNLELSPE GEEQESLLQPDQPSPEFTFQYDPSYRSVREIREHL RARESAESESWSCSCIQCELKIGSEEFEEFLLMD KIRDPFIHEISKIAMGMRSASQFTRDFIRDSGVVS LIETLLNYPSSRVRTSFLENMIHMAPPYPNLNMI TFICQVCEETLAHSVDSLEQLTGNKGCFRHLTMT IDYHTLIAN*YGPGFLLF*PQAQCGETKFHVLC MLLNLSENPAVAKKLFSAKALSIFVGLFNIEETN DNIQIVIKMFQNISNIKSGKMSLIDDDFSLEPLISA FREFEELAKQLQAQIDNQNDPEATGTTAFVGKG NNPSANRERLSPSVFCPGAQEAESLPARRVRGEE QRLLLEEVGARTADGIPEGW
3733	A	2	3274	DVPLIRIEEDTGEIFTTGARIDREKLCAGIPRDEHC FYEEVAILPDEIFRLVKIRFLIEDINDNAPLFPAT VINISIPENSAINSKYTLPAAVDPDVGINGVQNYE LIKSQNFGLDVIETPGGDKMPQLIVQKELDREK DTYVMKVKVEDGGFPQRSSTAILQVSVTDNDN HPVFKETEIEVSIPENAPVGTSTVQLHATDADIGE NAKIHFSFSLVSNIRRLFHLNATTGLITIKEPLD REETPNHKLVLASDGGMLPARAMVLVNVTDV NDNVPSIDIRYIVNPVNDTVVLSNIPNLTKIALIT VTDKADAHNGRVTCFTDHEIFRLRPVFSNQFLL ETAAYLDYESTKEYAIKLLA\ADAGKPPLNQSAM LFKVKDENDNAPVFTQSFVTVSIPENNSPGIQLT KVSAMDADSGPNKINYLGLPDAPPEFSLDCRT GMLTVVKKLDREKEDKYLFTILAKDNGVPPLTS NVTVFVSIIDQNDNSPVFTHNEYNFYVPENLPRH GTVGLITVTDPDYGDNSAVTSLILDENDDFTIDSQ TGVIRPNISFDREKQESYTFYVKAEDGGRVSRSSS AKVTINVVDVNDNKPVFIVPPSNCSYELVLPSTN PGTVVFQVIAVDNDTGMNAEVRYIVGGNTRDL FAIDQETGNITLMEKCDVTDGLHRLVKANDL GQPDLSLFSVIVNLFVNESVTNATLINELVPQKH LKHQ*PQILEIADVSSPTS DYVKILVA AVAGTITV VVVIFITAVVRCRQAPHLKAAQKNMQNSEWATP NPENRQMIMMKKKKKKKKKHSPKNLLNVVTIEE TKADDVDSGDNRVTLDPIDLEEQTMGKYNWV TPTTFKPDSPDLARHYKSASPQAFQIQPETPLN LKHIIQELPLDNTFVACDSISNCSSSSSDPYSVSD CGYPVTTTFEVPVSVHTRPPVDLEVGAQSGQVAI LTSSLMELLCLMVA AFLPLELRPLGQQNVMSW EQEAKILLVGYWGDGEWCHFHFHHLIPGPVNPG YERKQYHILDSSEDTQPSGELCPIPVRPFTILSIQ LLQDDGEHCGTKQGFPQAVQLGLLPHKTLK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3734	A	1	840	GTRPGHLPAPSDGFCV/HL*SIPSWGSEF*GESL/EM QLITSLGLQEFDIARNVLELIYAQTLVWIGIFFCPL LPFIQMIMLFIMFYSKNISLMMNFQPPSKA WRAS QMMTFFIFLLFFPSFTGVLCTLAITWRLKPSADC GPFRGLPLFIHSIYSWIDTLSTRPGYLWVWVIYRN LIGSVHFFILTIVLIITYLYWQITEGRKIMIRLLH EQINEGKDKMFLIEKLIKLDMEKKANPSSLVLE RREVEQQGFLHLGEHDGSLDLRSRVSQEGNPR A
3735	A	2	432	VEVCRRYLWKMTVDASQNVQCCVIFSHFPFIFN NLISKIKLLHTDTLLKIESKKHKA YLRSAIEEERE SEFALRPTFDLTVRRNHLIEDVLNQLSQFENEDL RKELWVSFSGEIGYDLGGS/VKKEIFYCLFAEMIQ PEYGMFMY
3736	A	1542	343	KGAPSFVRLYQYPNFAGPHAALANKSFFKADKV TMLWNKKATAVLVIASDVKDGTGASYYGEQTL HYIATNGESAVVQLPKNGPIYDVVWNSSTEFCA VYGFMFAKATIFNLKCDPVDFGTGPRNAAYYS PHGHIL VLAGFGNLIQI*AD/IMKVWNVKNYKLI SKPVASDSTYFAWCPDGEHILTATCAPRLRVNN GYKIWHYTGSIHLYDVPNAELWQVSWQFLD GIFPAKTITYQAVPSEVPNEEPKVATAYRPPALRN KPITNSKLHEEEPPQNMKPQSGNDKPLSKTALKN QRKHEAKKAAKQEARSDKSPDLAPTPAQSTPR NTVSQSISGDPEIDKKIKNLKKKLKAIEQLKEQAA TGKQLEKNQLEKIQKETALLQELEDLELGI
3737	A	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEE EILPEPGSETPTVASEALAELLHGALLRRGPEMG YLPGPPLGPEGGEEETTTTITTTTITTTTITTTT NNNISEGEGYVESPDLGSPVSRITLGLLDCTYSIHV YPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAP RLLANSSMLGEGQVLRSPITNRLLLHFQSPRVRG GGFRIHYQAYLLSCGFPPRAHGDVSVTDLHPGG TATFHCDSGYQLQGEETLCLNGTRPSWNGETPS CMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCR WVIEAAEGRRLLHLHFERVSLDEDNDRLMVRSGG SPLSPVIYDSMDMDVPERGLISDAQSLYVELLSET PANPLLLSLRFEAFEDRCFAPFLAHGNVTTTDPPE YRPGALATFSCPLGYALEPPGPPNAIECVDPTEPH WNDTEPACKAMCGGELSEPAGVVLSPDWQSY SPGQDCVWGVHVQEEKRILLQVEILNVREGDML TLFDGDGPSARVLAQLRGPQPRRRLSSGPDLT QFQAPPGPNNPGLGQGFVLHFKEVPRNDTCPELP PPEWGWRTASHGDLIRGTVLTYQCEPGYELLGS DILTCQWDLWSAAPPACQKIMTCADPGEIANG HRTASDAGFPVGVSHVQYRCLPGYSLEGAAMLTC YSRDTGTPKWSDRVPKCALKEYECLNPGVPENG YQTLKYHHYQAGESLRFYCYEGFELIGEVTITCV PGHPSQWTSQPPLCKVTQTTDPSRQLEGGNLAL AILPLGLVIVLGSQVYIYYTKLQGKSLFGFSGSH SYSPITVESDFSNPLYEAGDTREYEVSI
3738	A	3190	664	VAMGTPRAQHPPPPQLLFLILLSCPWIQGLPLKEE EILPEPGSETPTVASEALAELLHGALLRRGPEMG YLPGPPLGPEGGEEETTTTITTTTITTTTITTTT NNNISEGEGYVESPDLGSPVSRITLGLLDCTYSIHV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				YPGYGIEIQVQTLNLSQEEELLVLAGGGSPGLAP RLANSSMLGEGQVLRSPNRLLLHFQSPRVPRG GGFRIHYQAYLLSCGFPPRAHGDVSVTDLHPGG TATFHCDSGYQLQGEETLCLNGTRPSWNETPS CMASCGGTIHNA TLGRIVSPEPGGAVGPNLTCR WVIEAAEGRRRLHLHFERVSLDEDNDRLMVRSGG SPLSPVIYDSDMDDVPERGLISDAQSLYVELLSET PANPLLLSLRFEAFEDRCFAPFLAHGNVTTTDP YRPGALATFSCLPGYALEPPGPPNAIECVDPT WNTTEPACKAMCGGELSEPAGVVLSPDWQSY SPGQDCVWGVHVQEEKRILLQVEILNVREGDML TLFDGDGPSARVLAQLRGPQPRRRLSSGPDLT LQFQAPPGPPNPGLGQGFVLHFKEVPRNDTCPELP PPEWGWRTASHGDLIRGTVLTYQCEPGYELLGS DILTCQWDLWSAAPPACQKIMTCADPGEIANG HRTASDAGFPVGS HVQYRCLPGYSLEGAAMLTC YSRDTGTPKWSDRVPKCALKEYECLNPGVPENG YQTLYKHHYQAGESLRFCEYEGFELIGEVTITCV PGHPSQWTSQPPLCKVTQTTDPSRQLEGGNLAL AILPLGLVIVLGS GYIYYTKLQKSLFGFSGSH SYSPITVESDFSNPLYEAGDTREYEVSI
3739	A	734	445	LLEPEPAEEYTEQSEVEST/EGMILI*CCLYFAAFQ TNVSNIFYALQYVNRQFMAETQTSGEKEQVDE WTVETVEVRVLCIAKLLSLSSVS NFYLY
3740	A	2	1578	MAHYITFLCMVLVLLQNSVLAEDGEVRSSCRT APTDLVFILDGSYSVGPFENFEIVKKWLVNITKNF DIGPKFIQVG VVQYSDY PVLEIPLGSYDSGEHLTA AVESILYLGNTKTGKAIQFALDYLFKSSRFLT KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIG VGSETEDAELRAIANKPSSTYVFYVEDYIAISKIR EVMKQKLCEESVCPTRIPVAARDERGF DILLGLD VNKKVKKRIQLSPKKIKGYEVT SKVDLSELTSNV FPEGLPPSYV FVSTQRFKVKKIWDLWRILTIDG/* PQIAVTLNGVDKILLFTTTSVINGSQVVT FANPQV KTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPL HPVLGILINGQTQIGKYS GKEETVQFDVQKLRIY CDPEQNNRETACEIPGFCLNGPSDVGSTPAPCICP PGKPG LQGPKGDPGLPGNPGYPGQPGQDGKPV TESLVISGISGITGYQGIAGTPGVPGSPGIQGARGL PGYKGEPRDGDGK
3741	A	5048	1236	MSAPAGSSHPAASARIPPKFGGSAVSGAAAPAGP GAGPAPHQQNGPAQNQM VPSGYGLHHQNYIA PSGHYSQGP GKMTSLPLDTQCGDYYSALYTVPT QNVTPNTVNQQPGAQQLYSRGPPAPHIVGSTLGS FQGAASSASHLHTSASQPYSSFVNHNYS PAMYS ASSSVASQGF PSTCGHYAMSTVSNAAYPSVSYP LPAGDTYGMFTSQNAPT VRPVKDNFSFGQNTA ISHPSPLPPLPSQQHHQQSLSGYSTLTWSSPGLP STQDNLIRNHTGSLAVANNNTITVADSLSCPVM QNVQPPKSSPVVSTVLSGSSGSSSTRPTANHPV EPVTSVTQPSSELLQKGVQYGEYVNNQASSAPT PLSSTDDEEEEEDEEAGVDSSTTSASPMPS YDALEGGSPDMLSSASSAPDPAPEPD PASAP APASAPAPVVPQPSKMAKPLAMAIQHFSLVIRML QHHLFLEYSPSNPVYSGFQQYPQQYPGVNQLSSS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				IGGLSLQSSQPESLRPVNLTQERNILPMTVPVWAP VPNLNADLKKLNCSPDSFRCTLTNPQTQALLNK AKLPLGLLLHPFRDLTQLPVITSNTIVRCRSCRTYI NPVFVSFIDQRR*KCNLCYRVNDVPEEFMYNPLT RSYGEPHKRPEVQNS\TVEFIASSDYMLRPPQPAV YLFVLDVSHNAVEAGYLT/LWCQSLLNLDKLP G\DSRT\RIGFMTFD\STYSFLQFTQEGLSQPQMLI VSDIDDVFLPTPDSLLVNLYESKELIKDLLNALPN MFTNTRETHSALGPALQAAFKLMSPTGGRVSVF QTQLPSLGAGLLQSREDPNQRSSTKV VQH LGPAT DFYKKLALDCSGQQTAVDLFLLSSQYSDLASLA CMSKY SAGCIYYPSFHYTHNPSQAEKLQKDLK RYLTRKIGFEAVMRIRCTKGLSMHTFHGNFFVRS TDLLSLANINPDAGFAVQLSIEESLTDTSLVCFQT ALLYTSSKGERRIRVHTLCLPVVSSLSDVYAGVD VQAAICLLANMAVDRSVSSSLSDARDALVNAV DSLSAYGSTVSNLQHSALMAPSSLKLFPLYVLAL LKQKAFRTGTSTRLDDR VYAMCQIKSQPLVHLM KMIHPNLYRIDRLTDEGA VHVNDRIVPQPPLQKL SAEKL TREGAFLMDCGSVFYI WVKGCDNNFIT DVLGYTNFASIPQKMTHLPELDTLSSERARSFIT WLRDSRPLSPILHIVKDESPAKAEFFQHIEDRTE AAFSYEFLLHVQQQICK
3742	A	934	68	SMLASQGVLLHPYGVPMIVPAAPYLPGLIQGNQE AAAAPDTMAQPYASAQFAPPQNGIPAEYTAPHP HPAPEYTGQTTVPEHTLNLYPPAQTHSEQSPADT SAQTVSGTRNKQD* RSTDGWSPKQTQTS*KHGK QVSSPSGLHVSNIFFR\FRDPDLRQMFQGFQKILD VEIIFNERGSKGFGFVTFENSADADRAREK\ LHGT VV\EGRKIEVNN\NATARVMTNKKTVNPTYNGWK LNPVVGAVYSPEFYAGTVLLCQANQEGSSMYSA PSTDFRGAKLHTSRPLLSGS
3743	A	3	1456	QFQQA WMQNKVPIAPNEVLNDRKEDIKLEEK KTQAEIEQEMATLQYTNPQLLEQLKIERLAQKQV EQIQPPSSGTPLLGPQFPFGQGPMSQIPQGF/PTA PSISADANEHGSKGPPGPQGQFRPPGPQGGMGP QGPPLHQGGGGPQGFMGPPQGPQGPGLPRPD MHGPQGMQRHPGPHGPLGPQGPQGPQSSGPQG HMGPPQGPQGHIGPQGPQGPQGLGFPQGPPT QGMQGPQGPQGMQGPQGPQGPQGPQGPQGP VSQGPLMGLNPKGMQGPQGPQGPQGPQGPQGP MGHPPQEMRGPHPPGGLGHGPQEMRGPPQEI MQGPPQGSMLGPPQELRGPPQGSQSQGPQGPQGS GPPQGGMQGPQGPQGPQGPQGPQGPQGPQGPQ QKQTPLLGDGPAPFNQEGQSTGPPPLIPGLGQQ GAQGRIPPLNPGQGPQGPQGPQGPQGPQGPQGP PPRGRDGFPGPMKTLV
3744	A	1571	652	PLTGRKCPGWTHSGSRSPRIAEVPGFPKRAEA SRQFSETADRLELLRRVMAAAARATTPADGEEP APEAEALAAARERSSRFLSGLELVKQGAEARVFR GRFQGR\AAVIKHRFPKGYRHPALEARLGRRRTV QEARALLRCRRAGISAPVVFVDYASNCLYMEEI EGSVTVRDA\FSPLWRLKKTQGLSNLAKTIGQVL ARMHDEDLIHGDLTTSNMLLKPPLEQLNIVLIDF GLSFISALPEDKGVLDLYVLEKAFLSTHPNTETVFE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				AFLKSYSTSSKKARPVLKKLDEVRLRGKKRSMV G
3745	A	127	1433	GSHRFSLASPLDPEVGPYCDTPTMRTLFLNLLWLA LACSPVHTTSLKSDAKKAASKTLLEKSQFSDKPV QDRGLVVTDLKAESVLEHRSYCSAKARDRHFA GDVLGYVTPWNSHGVDVTKVFGSKFTQISPVWL QLKRRGREMFVETGLHDVDQGWMAVRKHAK GLP*CLGSLRTGLTMISG/YVLDSEDEIEELSKT VVQVAKNQHFDFGVVEVWNQLLSQKRVGLIHM LTHLAEALHQAALLVIPPATPGTDQLGMFT HKEFEQLAPVLDGFSLMTYDYSTAHPGPNAFL SWVRACVQVLDPKSKWRSKILLGLNFYGM DY A TSKDAREPVVGARYIQTLDHRPRMVWDSQVSE HFFEYKKSRSGRHVVFPYPTLKSQVRLERELG VGVSIEWELGQGLDYFYDLL*VGIAASADVFFSK PWSE
3746	A	1	898	IDRAAECRTKPLPMAVSIRGNADSIVACLVMVL YLIKKRLVACAAVFYGFVHMKIYPETYILPITL HLLPDRDNDKSLRQFRYTFQACL*ELLKRLCNR TALMFVAVAGLTFALSFGFYEYGEFLEHTYF YHLTRDIRHNFSPYFYMLYLTAEKWSFSLGIA AFLPQLILLSAVSFAYYRDLVFCWFLHTSIFVTN KVCTSQYFLWYLCLLPLVMPLVRMPWKRAVVL LMLWFIGQAMWLAPAYVLEFQGKNTFLFIWLA GLFLLINCSILIQIISHYKEEPLTERIKYD
3747	A	1	2325	MVISFQGLVTFGDVAVDFSQEEWEWLNPIQRNL YRKVMLENYRNLASLGLCVSKPDVISSLEQGKEP WTVKRMTRA WCPDLKA VWKIKELPLKDFCE GKLSQAVITERLTSYNLEYSLLGEHWYDADFET QPGLVTIKNLAVDFRQQLHPAQKNFCKNGIWEN NSDLGSAGHCVAKPDLVSLLEQEKEPVMVKREL TGSLSFGQRSVHETQELFPKQDSYAEGVTDRTSN TKLDCSSFRENWDSYVFGRLAVGQETQFRQE PITHNKTLSKERERTYNKSGRWFLYDDSEEKVVH NRDSIKNFQKSSVVIKQTGIYAGKKLFCNECKK TFTQSSSLTVHQRIHTGEKPYKCNECGKAFSDGS SFARHQRCHTGKKPYECIECGKAFIQNTSLIRHW RYYHTGEKPFDCIDCGKAFSDHIGLNQHRIHTG EKPYKCDVCHKSFRYGSSLTVHQRIHTGEKPYE CDVCRKAFSHHASTQVHQRVHSGEKPFCKCEC GKAFRQNIHLASHLRIHTGEKPFCEAECGKSFSIS SQLATHQRIHTGEKPYECKVCSKAFTQKAHLAQ HQKTHTGEKPYECKECGKAFSQTTHLIQHQRVH TGEKPYKMECGKAFGDNSSCTQHQLHTGQRP YECIECGKAFKTKSSLICHRRSHTGEKPYECSVC GKAFSHRQSLSVHQRIHSGKKPYECKECKRTFIQI GHLNQHKRVHTGERSYNYKSRKVFRQTAHLA HHQRIHTGESSTCPSLPSTSNPVDLFPKFLWNPSS LPSP
3748	A	823	1	GGYTKSGYDSACKDFVPHDLEVQIPGRVFLVTG GNSGIGKATALEIAKRGGTVHLVCRDQAPAEDA RGEIIREISGNQNIHLHIVDLSDPKKIWKVENFKQ EHKLHVLVNNAGCMVNKREAHKKMDFEKNFG CQYSGVCTFLTTRPDPLCWRKNTDPRVITVSSG GMLVQKLNNQ*SPVRKNTIWMGMTMVYAQNKVS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ERQQVVLTERWGPAPG\IHFSSMHPGWA\DTGP VRQAMPGFHVQASGYRLRSEAQGADTMLWLAL SSARSRTAQR
3749	A	1939	715	GFLRLSQATRQRLSIPVMVLTLDPTRD\QCFGDR FSRLLLDEFLGYDDIL\MSSVKGLAENEENKGFLR NVVSGEHYRFV\SMWMARTSYLAAFANHGQSF T\SVSHACCGYSHHQIFVFVDLLQMLEMNMAIA FPAAPLLTVILALVGM\AIMSEFFNDTTTAFYIILI VWLADQYDAICCHTSTSKRH\WLRFFYL\YHFAFY AYHYRFNGQYSSLALVTSWLFQ\HSMIYFFHHYE LPAILQH\VRIQ\EMLLQAPTLGPGTPTA\LPDDMN NNSGAPATAP\DSAGQPPALGPVSPGASGSPGPV AAAPSSLVAAAA\SVAAAAGGDLGWMAETAAIIT DASFLSGLSASLLERRPASPLGPAGGLPHAPQDS VPPSDSAASD\TTPLGAAVGGPSPASMAPTEAPSE VGS
3750	A	2	844	GLLEPFSKLLSFVIQNAVFTLAYLVELCGLCYRA FTKERDKFYLSRSVVLELLQALKLKSPLPDTNLL LLVQFICADAGTKLAESTILSKQM\IASVPGCGTA AMECVRQYINEVLD\FMADMHTLTKLKSHMKT SQPLHEDTFGGHLKVGLAQIAAMD\ISRGNHDR KAVIRYLPWLYHPPSAMQQGPK\EFIECVSHIRLL SWLLGSLTHNAV\CKWPPLPGLPIPLDAGSHV ADHLIVILIGFPEQSKTSV\HMC\SLFHAFSLAQL WDSLLARQSGRW
3751	A	431	2	AFTRKCEETA\FIVPQCEI\IPE/WVCCR\IPTGSSLER NPGVKEGCEFCPPKVEMFFKDDAN\HDPQWSRQ QLIAAKFGFAALGI/QTEVDIMSHAT*AVFEIPEKS RLAPQNC\TPVDMKIEFGVHVTSKEILTDVIDNDS* RHSPS
3752	A	131	1278	AWSGSGLLVLCINTASMPMISVLGKMF\WQREG PGGRWTCQTSRRVSSDPAWA\VEWIELPRGLSLSS LGSARTLRGWSR\SSRPSSVDSQDLPEVNVGDTV AMLPKSRRALTIQEIAALARSSLHG\ISQVVKDHV TKPTAMAQGRVAHLIEWKGWSKPSDSPA\ALES FSSYSDLSEGEQEARFAAGV\AEQFAIAEAKLRA WSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPL GPHLQDLFTGHRFSRPVRQGSVEPESDCSQT\VP DTLCSSLC\SLDGLLGSPARLA\PCSWAMSCFSPN CPPAGKVPSAAW/APLEAQDSL\YNSPLTESCLSP AEEEPAPCKDCQPLCPPLTGSWERQRQASDLASS GVVSLDEDEAEPEEQ
3753	A	3	1138	YYSSVRQRVTCEEPRFRECAAA\IEGSATEVYAG EWRADRRSGFGVSQRSNGLRYEGEWLGNRRHG YGR\TTRPDGSREEGKYKRNLVHGGRVRSLLPL ALRRGKVKEKVDRAVEGARRAVSAARQRQEIA AARAADALLKAVAASSVAEKAVEAARM\AKLIA QDLQPMLEAPGRRRPRQDSEGS\DTPELDEDSGPV YENGLTPSEGSPELPSSPASSRQPWRPPACRSPLP PGGDQGPFFSPKAWPEEWGGAGAQAEELAGYE AEDEAGMQGPGRDGSPLLGGCSDSSGSLREEE GEDEEPLPPLRAPAGTEPEPIAMLVLRGSSSRGPD AGCLTEELGEPAATERPAQPGAANPLVVG\AVAL LDLSLAFLFSQLLT
3754	A	2	3338	SSLLEKMTSSDKDFR\FMATSDLMSELQKDSIQLD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EDSERKVVVKMLLRLLLEDKNGEVQNLAVKWLGV PLGAFHASLLHCLLPQLSSPRLAVRKRAVGALGH LATACTDLFVELADHLLDRLPGPRVPTSPTAIRT LIQCLGSVGRQAGHRLGAHLDRVLVLEDVFCNL DDDELRESCLQAFEAFLRKCPKEMGPHVPNVTS LCLQYIKHDPNPNYDSDEDEEQMETEDSEFSEQE SEDEYSDDDDMSWKVRRAAAKCIAALISSRPDL LPDFHCTLAPVLIRRFKEREENVKADVFTAYIVL LRQTRPPKGWLEAMEEPTQTGSNLHMLRGQVPL VVKALQRQLKDRSVRARQGCFSLLTELAVGLPG SLAEHMPVLVSGIIFSLADRSSSTIRMDALAFLQ GLLGTEPAEAFHPLPILLPPVMACVADSFYKIA AEALVVLQELVRALWPLHRPRMLDPEPYVGEMS AVTLARLRATDLDQEVKERAISCMGHLVGHLGD RLGDDLEPTLLLLLDRLRNEITRLPAIKALTLVAV SPLQLDLQPILAEALHILASFLRKNQRALRLATLA ALDALAQSGLSLPPSAVQAVLAELPALVNESD MHVAQLAVDFLATVTQAQPASLVEVSGPVLSEL LRLRSPLLPAGVLAAAEGLQALVGTRPPCVDY AKLISLLTAPVYEQAVDGGPGLHKQVFHSLARC VAALSAACPQEAESTASRLVCDARSPHSSTGVK VLAFLSLAEVGQVAGPGHERELKAVLLEALGSPS EDVRAAASYALGRVGAGSLPDFLPFLLEQIEAEP RRQYLLLHSLKEALGAAQPDLSKPYAEDIWALL FQRCEGAEEGTRGVVAECIGKLVVNPSFLLPRL RKQLAAGRPHTRSTVITAVKFLISDQPHPIDPLLK SFIAVHNKPSLVRDLDLPLLYQETKIRRDIRE VEMGPFKHTVDDGLDVRKA AFECMYSLLESLCG QLDICEFLNHVEDGLKDHYDIRMLTFIMVARLAT LCPAPVLQRVDRLIEPLRATCTAKVKAGSVKQEF EKQDELKRSAMRAVAALLTIPEVGKSPIMADFSS QIRSNPELAALFESIQKDSTSAPSTDSMELS
3755	A	2	3338	SSLLEKMTSSDKDFRSMATSDLMSELQKDSIQDL EDSERKVVVKMLLRLLLEDKNGEVQNLAVKWLGV PLGAFHASLLHCLLPQLSSPRLAVRKRAVGALGH LATACTDLFVELADHLLDRLPGPRVPTSPTAIRT LIQCLGSVGRQAGHRLGAHLDRVLVLEDVFCNL DDDELRESCLQAFEAFLRKCPKEMGPHVPNVTS LCLQYIKHDPNPNYDSDEDEEQMETEDSEFSEQE SEDEYSDDDDMSWKVRRAAAKCIAALISSRPDL LPDFHCTLAPVLIRRFKEREENVKADVFTAYIVL LRQTRPPKGWLEAMEEPTQTGSNLHMLRGQVPL VVKALQRQLKDRSVRARQGCFSLLTELAVGLPG SLAEHMPVLVSGIIFSLADRSSSTIRMDALAFLQ GLLGTEPAEAFHPLPILLPPVMACVADSFYKIA AEALVVLQELVRALWPLHRPRMLDPEPYVGEMS AVTLARLRATDLDQEVKERAISCMGHLVGHLGD RLGDDLEPTLLLLLDRLRNEITRLPAIKALTLVAV SPLQLDLQPILAEALHILASFLRKNQRALRLATLA ALDALAQSGLSLPPSAVQAVLAELPALVNESD MHVAQLAVDFLATVTQAQPASLVEVSGPVLSEL LRLRSPLLPAGVLAAAEGLQALVGTRPPCVDY AKLISLLTAPVYEQAVDGGPGLHKQVFHSLARC VAALSAACPQEAESTASRLVCDARSPHSSTGVK VLAFLSLAEVGQVAGPGHERELKAVLLEALGSPS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EDVRAAASYALGRVGAGSLPDFLPFLLEQIEAEP RRQYLLLHSLKEALGAAQPDLSKPYAEDIWALL FQRCGAEEGTRGVVAECIGKLVLVNPSFLLPRL RKQLAAGRPHTRSTVITAVKFLISDQPHPIDPLLK SFIAVHNKPSLVRDLLDDILPLLQETKIRRDILIRE VEMGPFKHTVDDGLDVRKAAFECCMYSLLESCLG QLDICEFLNHVEDGLKDHYDIRMLTFIMVARLAT LCPAPVLQRVDRLIEPLRATCTAKVKAGSVKQEF EKQDELKRSAMRAVAALLTIPEVGKSPIMADFSS QIRSNPELAALFESIQKDSAPSTDSMELS
3756	A	112	1361	SLEEQQGRHPSFAPKCAEQILGRIMITLITEQLQK QTLDELKCTRFSSISLPLPDHADISNCGNSFQLVSE GASWRGLPHCSCAEFQ/DQPQLQLPSLRPEPAPQ TTHRGNSPKEQPFQSVLRPEPPDPEKLPVPPAPPS KRHCRSLSPVDLSRWQPVWRPAPSKLWPIKH RGSGGGGGPQVPHQSPPKRVSSL/SVPPSSQCLFS MCPSSHTLQPSFLOPGPGADSSRPCAASPOSGSW ESDAESLSPCPPQRRFSLSPSLGPQASRFLPSARSS PASSPELPWRPRGLRNLPSSRSQPCDLDDARKTG VRRHEEDPRRLRPSLDFDKMNQKPYSGGLCLQE TAREGSSISPPWFMA CSPPLSASCSTGGSSQVL SEEEEEEGA VRWGRQALSKRTLQCRDFGDLNL NLIEN
3757	A	413	1	PKPMLQQDFT/SLPDQGLDHIAE/NSYFDARSLCA AELVCKEWQQVTSE*MLWKKLIERMVHAYPLW KGLSEKVV/DQHLFKNRPTDGPPNSFHRSLYPKII QVIETIESNWQCG*HTLQRIQCHSEKSKGVYCLQ YDEK
3758	A	2	613	FVSGSPWRMDGSTERLEARRPAGRLPWSSRQEM TRRPSLMAGRQHGWSAQQSATVANPVPGANPD LLPHFLGEPEDVYIVKNKPVLLVCKAVPATQIFF KCNGEWVRQVDHVIERSTDGSSGLPTMEVRINV SRQQVEKVFGLEEYWCQCVAWSSSGTTSQKA YIRIAYLRKNFEQEPLAKEVSLEQGIVLPCRPEGI PPAE
3759	A	1	561	ADDTLHLWNLROKRPAILHSLKFCRERVTFCHLP FQSKWLYVGTERGNIHVNVEFTLSGYVIMWN KAIELSSKSHPGPVVHISDNPMDEGKLLIGFESGT VVLWDLKSKKADYRYTYDEAIHSAWHHEGKQ FICSHSDGTLTIWNVRSPAKPVQTITPHGKQLKD GKKPEPCKPILKVEFXTTR
3760	A	1	824	LPACRCGCVAGCPSNHGICRCLRASERQVCVMH LKHLRTLLSPQDGAQKVTCAWSQNNAKFAVC TVDRVVLLYDEHGERRDKFSTKPADMKYGRKS YMVKGMAFSPDSTKIAIGQTDNIYVYKIGEDWG DKKVICNKFQITVKFRPVPGTLG*TNIQYIYL*IQ PGVAFLTSECDFSYCKDGASWLFMVICCLP*SPA VSFPIGD*ISAVTCLQWPAEYIIVFGLAEGKVRLS NTKINKSSTIYGTESYVVSLLTNCSGKGILSGHA DGYQR
3761	A	2253	320	PVIQRCSQPYGFSLLISFFLKCVSETSQQPPSRKVF QLLPSFPTLTRSKSHESQLGNRIDDVSSMRFDLSH GSPQMVRDGLSVTHRFSTKSWLSQVCHVCQK SMIFGVKCKHCRKCKHNKCTKEAPACRISFLPLT RLRRTESVPSDINNPNVDRAAEPHFGTLPKALTKK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EHPPAMNHL DSSSNPSSTTFSTPSSPAPFTSSNPS SATTPP\NPSP\GQR\DSRFNFPS C\AYFIHHR\Q\QFI FPDISAFAHAAPLEAADGTRLDDQPKADVLEAH EAEAEPEAGKSEAEDDEDEVDDLPSRRPWG PISRKASQTSVYLQEWDPFEQVELGEPGQGRW GRVHRGRWHGEVAIRLLEMDGHNQDHLKLFKK EVMNYRQTRHENVVLFMGACMNPPHLAIITSFC KGRTLHSFVRDPKTSLDINKTRQIAQEIIKGMGYL HAKGIVHKDLKSRNVFYDNGKVVITDFGLFGIS GVVPEGRRENQLKLSHDWLCYLAPEIVREMPG KDEDQLPFSKAADVYAFGTVWYELQARDWPLK NQAAEASIWQIGSGEGMKRVLTSSVLGKEVSEN LSACWAFDLQERPS\FSLMDMLEKLPKLNRRLS HPGHF*KSADINSSKVVPRFERFGLGVLESSNPK M
3762	A	2	1578	MAHYITFLCMVLVLLQNSVLAEDGEVRSSCRT APTDLVFILDGYSVSGPENFEIVKKWLVNITKNF DIGPKFIQVG VVQYSDYPVLEIPLGSYDSGEHLTA AVESILYLGNTKTGKAIQFALDYLFKSSRFLT KIAVVLTDGKSQDDVKDAAQAARDSKITLFAIG VGSETDAELRAIANKPSSTYVFYVEDYIAISKIR EVMKQKLCEESVCPT RIPVAARDERGF DILLGLD VNKKVKKRIQLSPKKIKGYEVTSKVDLSELTSNV FPEGLPPSYV FVSTQRFKVKKIWDLWRILTIDG/* PQIAVTLNGVDKILLFTTTSVINGSQVVT FANPQV KTLFDEGWHQIRLLVTEQDVTLYIDDQQIENKPL HPVLGILINGQTQIGKYSKEETVQFDVQKLRIY CDPEQNNRETACEIPGFCLNGPSDVGSTPAPCICP PGKPG LQGPKGDPGLPGNPGYPGQPGQDGKPV TESLVISGISGITGYQGIAGTPGVPGSPGIQGARGL PGYKGEPRDGDK
3763	A	3	1267	CKVWRNPLNLFRAEYNRYTWVTGREPLTYD MNLSAQDHQTFFTCDSDHLRPADAIMQKAWRE RNPQARISAAHEALEINECATAYILLAE EEA TTIA EAEKLFKQALKAGDGCYRRSQQLQHHGSQYEA QHSVLYLPLQ\TRHQCLGVHQQKASNVCQK TRE DQGSSENDERFNEGVPSEYVQYP*KPFKALLEL QAYADVQAVLAKYDDISLPKSATICYTAALLKA RAVSDKFSPEAASRRGLSTAEMNAVEAIHRAVEF NPHVPKYLLEMKSLLPPEHILKRGDSEAIAYAFF HLAHWKRVEGALNLLHCTWEGTFRMIPYPLEKG HLFYPPICTETADRELLPSFHEVSVPKKELPFFI LFTAGLCSFTAMLALLTHQFPELMGVFAKAVSV CLEGGLGEWMGKAKGIKAA
3764	A	25	1032	RSADGLCGNKDRERGNEFTRNQAAQEVVNP KKMKKKKYVNSGTVTLLSFAVESECTFLDYIKG GTQINFTVAIDFTASNGNPSQSTSLHYMSPYQLN AYALALTA VGEI IQHYDSKMFALGF GAKLPDP GRVSHEFPLNGNQENPSCCGIDGILEAYHRSRRT VQLYGPTNFAPVVTHVARNA AAVQDGSQYSVL LIITDGVISDMAQTKEAIVNGSKLPMSIIIVGVGQ AEFNAMVELDGDVRISSRGKLAERD VQFVPR DYVDRTGNHVL SMARLARDVLA EIPDQLVSYM KAQGIRPRSPPAATHSPSQSPARTPPACPLHTHI
3765	A	172	3456	LGMMDSPKIGNGLPVIGPGTDIGISSLHMVG YLG

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KNFDSA KVP SDEYCPACKEKGK LKALKTYRISFQ ESIFLCEDLQCIYPLGSKSLNNLISPDLEECHTPHK PQKRKSLESSYKDSL LANSKKTRNYIAIDGGKV LNSKHNGEVYDETSSNLPDSSGQQNPRTADSLE RNEILEADTVDMATTKDPATVDVSGTGRPSPQN EGCTSKLEMPLESKCTSFPAQALCVQWKNA YALC WLDCL SALVHSEELKNTVTGLCSKEESIFWRLL TKYNQANTLLYTSQ LSGVKDGDCKKL TSEIFAEI ETCLNEVRDEIFISLQPQLRCTLGDMESPVFAPFL LLKLETHIEKLFY SFSWDFECSQCGHQYQNRH MKSLVTFTNVIPEWHPLNAAHFGPCNNCNSKSOI RKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHFE GCLYQITSVIQYRANNH FITWLDADGSWLECDD LKGPCSERHKKFEVPA SEIHIVIERKISQVTDKE AACLP LKKTNDQHALSNEKPVSLTSCSVGDAAS AETASVTHPKDISVAPRTLSQDTAVTHGDHLLSG PKGLVDNLP LTL EETIQKTASVSQ LNSEAFLLEN KPAVENTGILKTNTLLSQESLMASVSAPCNEKLI QDQFVDISFSPQVVNTNMQSVQLNTEDTVNTKS VNNTDATGLIQGVKSVEIEKDAQ LKQFLT PKTEQ LKPERVTSQVSNLKKKETTADSQTTTSKSLQNS LKENQKKPFVGSWVKGLISRGASF MPLCVSAHN RNTITDLQPSVKG VNNFGGFKTKG INQKASHVSK KARKSASKPPPISKPPAGPPSSNGTAAHPHAHAA SEVLEKSGSTSCGAQLNHSSYGN GISSANHEDLV EGQIHKLRLKL RKKLKA EKKKLAALMSSPQSRT VRSENLEQVPQDGSPNDCE SIEDLLNELPYPIDIA NESACTTVPGVSLYSSQT HEEILAELLSPTPVSTE LSENGEGDFRYLGMGDSHIPPPVPSEFNDVSQNT HLRQDHNYSPTKKNPCEVQPD SLTNNACVRTL NLESPMKTDIFDEFFSSSALNALANDTLDLPHFDE YLFENY
3766	A	3	1622	AQQIVYRNVMLENYKNLVSLGYQLTKPDVILRL EKGEPPWLVERIEHQETHPDSETAFEIKSSVSSRSI FKDKQSCDIKMEGMARNDLWYLSLEEVWKCRD QLDKYQENPERHLRQVAF TQKKVLTQERVSESG KYGGNCLLPAQLVLREYFHKRDSHTKSLKHDLV LNGHQDSCASNSNECGQTF CQNIHLIQFARTHTG DKSYKCPDNDNSLTHGSSLGISKGIHREKPYECK ECGKFFSWRSNLTRHQLIHTGEKPYECKECGKSF SRSSHIGHQKTHTGEEPYECKECGKSFSWFSHL VTHQRTHTGDKLYTCNQCGKSF/VHSSRLIRHQR THTGEKPYECEPGKSFRQSTHLILHQRTHVRVR PYECNECGKSYSQRSHLVVHHRIHTGLKPFECKD CGKCFSSRSHLYSHQRTHTG EKPYECHDCGKSFS QSSALIVHQRIHTGEKPYECCQCGKAFIRKNDLIK HQRIHVGEETYKCNQCGIIFSQNSPFIVHQIAHTG EQFLT CNQCGTALVNTSNLIGYQTNHIRENAY
3767	A	3	1622	AQQIVYRNVMLENYKNLVSLGYQLTKPDVILRL EKGEPPWLVERIEHQETHPDSETAFEIKSSVSSRSI FKDKQSCDIKMEGMARNDLWYLSLEEVWKCRD QLDKYQENPERHLRQVAF TQKKVLTQERVSESG KYGGNCLLPAQLVLREYFHKRDSHTKSLKHDLV LNGHQDSCASNSNECGQTF CQNIHLIQFARTHTG DKSYKCPDNDNSLTHGSSLGISKGIHREKPYECK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ECGKFFSWRSNLTRHQLIHTGEKPYECKECGKSF SRSSHLIGHQKTHTGEEPYECKECGKSFSWFSHL VTHQRTHTGDKLYTCNQCGKSF/VHSSRLIRHQR THTGEKPYECPECGKSFRQSTHLHLHQRTHVRVR PYECNECGKSYQSRLVHHRIHTGLKPFECKD CGKCFSSRLYSHQRTHTGEKPYECHDCGKSFS QSSALIVHQRHTGEKPYECCQCGKAFIRKNDLIK HQRIHVGEETYKCNQCGIIFSQNSPFIVHQIAHTG EQFLT CNQCGTALVNTSNLIGYQTNHIRENAY
3768	A	185	2258	SIHKMSRKISKESKKVNISSLESEDISLETTVPTD DISSEEREKGVRITRQLIERKELLHNIQLLKIELS QKTMIDNLKVDYLTKEELEEKLNDALHQKQL LTLRLDNQLAFQKQDASKYQELMKQEMETILLR QKQLEETNLQLREKAGDVRRSLRDFELTEEYIK LKAFFPEDQLSIPEYVSVRFYELVNPLRKEICELQV KKNILAEELSTNKNQLKQLTETYEEDRKNYSEV QIRCQRLALELADTKLIQQGDYRQENYDKVKS ERDALEQEVIELRRKHEILEASHMIQTKERSELSK EVTLEQTVTLQKDKEYLNRQNMELSVRCAHE EDRLERLQAQLEESKKAREEMYEKYVASRDHY KTEYENKLHDELEQIRLKTNQEIDQLRNASREMY ERENRNLREARDNAVAEKERA VMAEKDALEKH DQLLDREYELQLSTESKVTFLHQSCLKSFESE RVQLLQEETARNLTQCQLECEKYQKKLEVLTKE FYSLQASSEKRITELQAQNSEHQARLDIYEKLEK ELDEIIMQTAEIENEDEAERVLFSGYGANVPTT AKRRLKQSVHLARRVLQLEKQNSLI/LKRSQTSK GPSNTAFTRSLTEANSLLNQTPPYRYLIESVRQ RDSKIDSLTESIAQL/ERKDVSNLNKEKSALLQTN GIKMAL\DL\DQLLNHP
3769	A	3	2297	DAAEFRVVADAMKVIGFKPEEIQT VYKILAILH LGNLKFVVDGDTPLIENGKVVSIIAELLSTKTD VEKALLYRTVATGRDIIDKQHTEQEASYGRDAF AKAIYERLFCWIVTRINDIEVKNYDTTIHGKNTV IGVLDIYGFEIFDNNSEFCINYCNEKLQQLFIQL VLKQEQEYQREGIPWKHIDYFNNQIIVDLVEQQ HKGIIAILDDACMNVGKVTDEMFLALNSKLGK HAHFSSRKL CASDKILEFDRDFRIRHYAGDVVYS VIGFIDKNKDTLFDQDFKRLMYNSSNPVLKNMWP EGKLSITEVTKRPLTAATLFKNSMIALVDNLASK EPYYVRCIKPNDKSPQIFDDDERCRHQVEYLGIL ENVRVRRAGFAFRQTYEKF LHYKMISEFTWPN HDLPSDKEAVKKLIERCGFQDDVAYGKTKIFIRT PRTLFTLEELRAQMLIRIVLFLQKVWRGTLARMR YKRTKAALTIIRYRRYKVKSYIHEVARRFHGVK TMRDYGKHVKWSPPKVLRFEALQTIFNRWR ASQLIKSIPASDLPQVRAKVA AVEMLKGQRADL GLQRAWEGNYLASKPDTPTSGTFVPVANELKR KDKYMNVLFSCHVRKVNRFKVEDRAIFVTDRH LYKMDPTKQYKVMKTIPLYNLTGLSVSNGKQDL VVFHTKDNKDLIVCLFSKQPTHESTRIGELVGVLV NHFKSEKRHLQVNVNTPVQCSLHGKCKTVSVE TRLNQPPDFTKNRSGFILSVPGN
3770	A	3	6276	HKVAAPDVVPTLDTVRHEALLYTWLAEHKPL VLCGPPGSGKTMTLFSALRALPDMEVVGLNFSS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ATTPELLLKTFDHYCEYRRTPNGVVLPVQLGK WLVLFCDENLPDMDKYGTQRVISFIRQMVEHG GFYRTSDQTWVKLERIQFVGACNPPTDPGRKPLS HRFLRHVPVVVVDYPGPASLTQIYGTFRAMLR LIPSLRTYAEPLTAAMVEFYTMSQERFTQDTQPH YIYSPREMTWVRGIFEALRPLETLPVEGLIRIWA HEALRLFQDRLVEDEERRWTDENIDTVALKHFP NIDREKAMSRPILYSNWLKDYIPVDQEELRDYV KARLKVIFYEELDVPVLVFNELVDHVLRIDRIFR QPQGHLLIGVSGAGKTTLSRFVAMNGLSVYQ IKVHRKYTGEDFDEDLRTVLRRSGCKNEKIAFIM DESNVLDSGFLERMNTLLANGEVPGLFEGDEYA TLMTQCKEQAQKEGLMLDSHEELYKWFTSQVIR NLHVFTMNPSSEGLKDRAATSPALFNRCVLNW FGDWSTEALYQVGKEFTSKMDLEKPNYIVPDYM PVVYDKLPQPPSHREAIVNSCVFVHQT LHQANA RLAKRGGR TMAITPRHYLDFINHYANLFHEKRSE LEEQQMHLNVGLRKIKETVDQVEELRRDLRIKS QELEVKNAAANDKLKMKVQDQQAEEKKVMMS QEIQEQLHKQQEVIAQKMSVKEDLDKVEPAVI EAQNAVKSIIKQHLVEVRSMANPPAAVKLALES ICLLLGESTTDWKQIRSIIMRENFIPTIVNFSAEIS DAIREKMKKNYMSNPSYNYEIVNRSLACGPMV KWAIAQLNYADMLKRVPLRNLQKLEDDAKD NQQKANEVEQMIRDLEASARYKEEYAVLISEAQ AIKADLA AVEAKVNRSTALLKSLAERERWEKT SETFKNQMSTIAGDCLLSAFAIYAGYFDQQMR QNLFTTWSHHLQQANIQFRTDIARTEYLSNADER LRWQASSLPADDLCTENAIMLKRFNRYPLIDPS GQATEFIMNEYKDRKITRTSFLDDAFRKNLESAL RFGNPLL VQDVESYDPVLNPVLNREVRR TGGRV LITLGDQDIDLSPSFVIFLSTRDPTVEFPDLC SRV TFVNFTVTRSSLQSQCLNEVLKAERPDVDEKRS LLKLQGEFQLRLRQLEKSLQALNEVKGRILDDD TIITLENLKREAAEVTRKVEETDIVMQEETVS QQYLPSTACSSYFTMESLKQIHFLYQYSLQFLL DIYHNVL YENPNLKGVT DHTQRLSIITKDLFQVA FNRVARGMLHQDHITFAMLLARIKLKGTVEPT YDAEFQHFLRGNEIVLSAGSTPRIQGLTVEQAEA VVRLSCLPAFKDLIAKVQADEQFGIWLDSSEPEQ TVPYLWSEETPATPIGQAIHRLLLIQA FRPDRLLA MAHMFVSTNLGESFMSIMEQPLDLTQIVGTEVKP NTPVLMCSVPGYDASGHVEDLAAEQNTQITSIAI GSAEGFNQADKAIN TAVKSGRWVMLKNVHLAP GWL MQLEKKLHSLQPHACFRLFLTMEINPKVPV NLLRAGRIFVFEPPPGVKANMLRTFSSIPVSRICK SPNERARLYFLLAWFHAIQERLRYAPLGWSK KY EFGESDLRSACD TVDTWLDDTAKGRQNISPDKIP WSALKTLMAQSIYGGRV DNEFDQRLNNTFLERL FTTRSFDFEKLACKVDGHKDIQMPDGIRREEFV QWVELLPDTQTPSWLGLPNNAERVLLTTQGV D MISKMLKMQMLEDDEDDLAYAETEKKTRTDSTS DGRPA WMR TLHTTASNWLHLIPQTL SHLKRTVE NIKDPLFRFFEREV KMGAKLLQDVRQDLADV V QVCEGKKKQTNYLRTLIINELVKGILPRSWSHY

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TVPAG\MTVIQWGVPI SARRIKQLQNISLAAAASG GAKELKNIHVCLGGLFVPEAYITATRQYVAQAN SWSLEELCLEVNVTTSSQATLDACSFVGTGLKL QGATCNNNKL SLSNAISTALPLTQLRWVKQTNT EKKASVVTLPVYLNFTRADLIFTVD F E IATKEDPR SFYERGVAVLCTE
3771	A	1	2043	LPLLHAGFNRRFMENSSIIACYNELIQIEHGEVRS QFKLRACNSVFTALDHCHEAIEITSDDHVIQYVN PAFERMMGYHKGELLGKELADLPKSDKNRADL LDTINTCIKKGKEWQGVYYARRKSGDSIQQHVKI TPVIGQGGKIRHFVSLKKLCCTTDNNKQIHKIHR DSGDNSTEPHSFRYKNRRKESIDVKSISRRGSDA PSLQNRRYPSMARIHSMTEAPITKVINIINAAQEN SPVTVAEALDRVLEILRTTELYSPQLGTKDEDPH TSDLVGGLMTDGLRRLSGNEYVFTKNVHQSHSH LAMPITINDVPPCISQLDNEESWDFNIFELEAITH KRPLVYLGLKVFSRFGVCEFLNCSETTLRAWFQ VIEANYHSSNAYHNSTHAADV LHATAFFLGKER VKGSLDQLDEVAALIAATVHDVDHPGRTNSFLC NAGSELAVLYNDTAVVLESHHTALAFQLTVKDT K\CNIFKNID/RGNHYRTL RQAIDMV LATEMTKH FEHVNK FVNSINKPMAAEIEGSDCECN PAGKNFP ENQILIKRMMIKCADVANPCRPLDLCIEWAGRIS EEYFAQTDEEK RQGLPVVMPV FDRNTCSIPKSI SFIDYFITDMFDAWDAFAHLPALMQHLADNYKH WKTLDLCKCKSLRLPSDRLKPSHRGGLLTDKGH CESQ
3772	A	1013	50	TLVHADGFP SLHITETCLAYREKRIGIDLVDHDTVE HELIKEAEIIQGIMALLTRTLEEASEQIRMNRSK YNLEKDLKDKFVALTIDDICFSLNNSPNIRYSEN AVRIEPNSVSLEDWLD F SSTNVEKADKQRNNSL MLKALVD\RILSQTANYLRKQCDVVHTAFKNGL KDTKDARDQLADHLAK\VMEEIASQEK NITALEK AILDQEGPAKVAHTRLETRTHRPNVELCRDVAQ YRLMKEVQEITHNVARLKETLA\QAQAE LKGLH RRQLALQEEIQVKENTYIDEVLCMQMRKSIPLR DGEDHGVWAGGLRPDAVC
3773	A	1	955	AAARESERQLRLRLCVLNEILGTERDYVGT LRF QSAFLHRIRQNVADSVEKGLTEENVKVLFSNIEDI LEVHKDFLALEYCLHPEPQSQHELGNVFLKFK DKFCVYEEYCSNHEKALRLVELNKIPTVRAFL SCMLLGGRKTTDIPLEGYL\LSPIQRICKYPLLLKE LAKRTPGKHPDHPAVQ\ S ALQAMKTVCSNINETK RQMEKLEALEAAA\QSHIEGWEGSNLTDICTQLL LQGTLLKISAGNIQERAFFLFDNLLVYCKRKS RV TGSKKSTKRKTSINGSLYIFRGRINTEVMEVENVE DGTGSPSPSLA
3774	A	4254	2061	ELQGDFSVPDVPKSMWCENSICVGFKR DYYLI RVDGKGSIKELFPTGKQLEPLVAPLADGK VAVG QDDLTVVLNEEGICTQKCALNWDIPVAMEHQ PYIIAVLPRYVEIRTFEPRLLVQSIELQRP RFI SGG SNIIYVASNHFWRLIPVPMATQIQQLLQDKQFE LALQLAEMKDDSDSEKQQQIHHIKNLYAFNLFC QKRFD ESMQVFAKLGTDP THVMGLYPDLLPTDY RKQLQYPNPLPVLSGAELEKAHLALIDYLTQKRS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				QLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQII DTLLKCYLHTNVALVAPLLRLNHNHCHIEESEH VLKKAHKYSELILYEKKGLHEKALQVLVDQSK KANSPLKGHERTVQYLQHLGTENLHLIFSYSVW VLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN FKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKV QGLMKEYLLSFPAGKTPVPAGEEEGELGEYRQK LLMFLEISSYYDPGRICDFPFDGLLEERALLGR MGKHEQALFIYVHILKDTRMAEEYCHKHYDRN KDGNDVYLSLLRMYLSPPSIHCLGPIKLELLEPK ANLQAALQVLELHHSKLDTTKALNLLPANTQIN DIRIFLEK VLEENAQKKRFNQVLKNLLHAEFLRV QEERILHQQVKCIITEEKVCMVCKKKIGNSAFAR YPNGVVVHYFCSKEVNPADT
3775	A	1832	839	MSRARGALCRACLALAAALAALLLPLPLPRAP APARTPAPAPRAPPSPAPASLRPDDVFIAVKTTT KNHGPRLRLLLRTWISRARQQTFFITDGDDEPELE LQGGDRVINTNCSAVRTRQALCCKMSVEYDKFI ESGRKWFCHVDDDNVYNARSLHLLSSFSQSQD VYLGRPSLDHPTEATERVQGGRTVTTVKFWFAT GGAGFCLSRGLALKMSPWASLGSFMSTAEQVRL PDDCTVGVIYEGLLGARLLHSPFLFHSLENLQRL PPDTLLQQVTLSHGGPENPQNVVNVAGGFSLHQ DPTRFKSIHCLLYPDTDWCPQKQGAPTSTR
3776	A	3	796	PRAKLGTRARNMAGQDAGCGRGDDYSEDEGD SSVSRAA VEVFGKLKDLNCPFLEGLYITEPKTIQE LLCSPSEYRLEILEWMCTRVWPSLQDRFSSLKGV PTEVKIQEMTKLGHELMMLCAPDDQELLKGCACA QKQLHFMDQLLDITIRSLTIGCSSCSLMEHFEDT REKNEALLGELFSSPHLQMLLNPECDPWPLDMQ PLLNKQSDDWQWASASAKSEEEKLAELARQLQ ESA AKLHALRTEYFAQHEQGAAGAANTSAP
3777	A	3	413	SEEDVIEGKTAVIEKRRKRSSAGVVED/IGGEVQ NMLEGVGV DINKALLAKRRKLEMYTKASLRTSN QKIEHVWK TQDQQRQKLNQEYSQQFLTFFQQW DLDMQKAEEQEEKILVGIMIRFIINQVSSRNGQPS LLL
3778	A	132	788	SRLPPPPHLDGRAGARVPR SARLSRWWVQD WTHGPIVRPPAAARTMWVNPEEVLLANALWITE RANPYFILQRRKGHAGDGGGGGGLAGLLVGTL D VVLDSARVAPYRILYQTPDSL VYWTIACGIGSR KEITEHWEWLEQNLLQTL SIFENENDITTFVRGKI QGIIAEYNKINDVKEDDDTEKFKEAIVKFHRLFG MPEEEKLVNYSCSYWKG
3779	A	2	934	CKSCTLFPQNPPLPPSTRERPPGCKTVFVGGLPE NATEEIIQEVFEQCGDITAIRKSKKNFCHIRFAEEF MVDKAIYLSGYRMRLGSSTDKKDSGRLHVDFA QARDDFYEWCKQRMRA REERHRRKLEEDRLR PPSPPAIMHYSEHEAALLAEKLDKDSKFSEAMQ VLLSWIERGEVNRRSANQFYSMVQSANSHVRL MNEKATHEQEMEEAKENFKNALTGILTQFEQIV AVFNASTRQKA WDHFSKAQRKNIDIWAKHSEE LRNAQSEQLMGIRREEEMEMSDDENCDSPTKKM RVDESALGAP
3780	A	1	2535	AAQAEREELAAGRMPGGGPQGAPAAAGGGGVS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				HRAGSRDCLPPAACFRRRLARRPGYMRSSSTGP GIGFLSPA VGT LFRFP GGVS GEESHSESRRARQC GLDSRGLLVRS PVSKSAAAPT VTSVRG TSAHFGI QLRGGTRL PDRLSWPCGPGSAGWQEF AAMD SETLDASWEAACSDGARRVRAAGSLPSAELSSNS CSPGCGPEVPPTPPGSHSAFTSSFSFIRLSLGSAGE RGEAEGCPPSREAESHCSQPQEMGAKAASLDGP HEDPRCLSQPFSLLATRV SADLAQAARNSSRPER DMHSLPDMDPGSSSSLDPSLAGCGGDGSSGSGD AHSWDTLLRKWEPVLRDCLLRNRRQMEVISRL KLQKLQEDAVENDDYDKAETLQQRLEDLEQEKI SLHFQLPSRQPALSSFLGHLAAQVQAALRRGATQ QASGDDTHPLRMEPRILEPTAQDSLHVSITRRD WLLQEKQQLQKEIALQARMFVLEAKDQQLRRE IEEQEQLQWQGC DLTPLVGQLSLGQLQEVSKA LQDTLASAGQIPFHAEPETIRSLQERIKSLNLSLK EITTKVCMSEKFCSTLRKKVNDIETQLPALLEAK MHAISGNHFWTAKDLTEEIRSLTSDREGLEGLLS KLLVLSSRNVKKLGSVKEDYNRLRREVEHQETA YETSVKENTMKYMETLKNKLCSCCKPLLKQVW EADLEACRLLIQCLQLQEARGSLSVEDERQMD LEGAAPPPIPRHLHSEDKRKTPLKESYILSAELGEK CEDIGKKLLYLEDQLHTAIHSHDEDLIQLSLRRELQ MVKETLQAMILQLQPAKEAGEREAAASCMTAG VHEAQA
3781	A	3	995	GRRRAGPAHSARMYNNMETELKPPGPQQTSGG GGGNSTAAAAGGNQKNSPDRVKRPMNAFMVW SRGQRRKMAQENPKMHNSEISKRLGAEWKLLSE TEKRPFIDEAKRLRALHMKHEHPDYKYRPRRRTK TLMKKDKYTLPGGLLAPGGNSMASGVGVGAGL GAGVNQRMDSYAHMNGWSNGSYSMMQDQLG YPQHPGLNAHGAAQMOPMHRVDVSALQYNM TSSQTYMNG/SRPTYSMSYSQQGTPGMAPGS/MG SVVKSEASSSPVVTSSSHSRAPCQAGDLRDMIS MYLPGAEVPEPAAPSRLHMSQHYQSGPVPGTAI NGTLPLSHM
3782	A	1	2649	FRVPDSCPVVLHSFTQLDPDLRPESSTQEIGEELI NGVIYSISLRKVQLHHGGNGQRWLG YENESAL NLYETCKVRTVKAGTLEKLVEHLVPAFQGS DLS YVTIFLCTYRAFTTTQQVLDLLFKRYGRCDALTA SSRYGCILPYSDGDPQDQLKNAISSILGTWLD QYSEDFCQPPDFPCLKQLVAYVQLNMPGSDLER RAHLLLAQLEHSEPIEAEPGEEDWALSPVPALK PTPLELALTPARAPSPVPAPAPEPEPAPTAPGSE LEVAPAPAPELQQAPEPAVGLESAPAPALELEPA PEQDPAPSQTLELEPAPAPVPSLQPSWSPVVAEN GLSEEKPHLLVFPPDLVAEQFTLMDAELFKKVVP YHCLGSIWSQRDKKGKEHLAPTIRATVTQFNSV ANCVITTCLGNRSTKAPDRARVVEHWIEVAREC RILKNFSSLYAILSALQNSIHLKKTWEDVSRDS FRIFQKLSEIFSDENNYLSRELLIKEGTSKFATLE MNPKRAQKRPKETGIIQGTVPYLGTFLTDLVML DTAMKDYL YGR LINF EKKRKEFEVIAQIKLLQSA CNNYSIAPDEQFGA WFAVERLSETESYNLSCEL EPPSESASNTLR TKNTAIVKRWSRQAPSTELS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				TSGSSHSKSCDQLRCGPYLSSGDIADALSVHSAG SSSSDVEEINISFVPESPDGQEKKFVESASQSSPET SGISSASSSTSSSSASTTPVAATRTHKRSVSGLCNS SSALPLYNQVGDCCIRVSLDVDNGNMYKSILV TSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILS DDRKLKIPENANVFYAMNSTANYDFVLKRTFT KGVKVKHGASSTLPRMKQKGLKIAKGIF
3783	A	3	869	RSGQGKVVYGLIGRRRFQQMDVLEGLNLLITISGK RNKLRVYYLSWLRNKILHNDPEVEKKQGWTTV GDMEGCGHYRVVKYERIKFLVIALKSSVEVYAW APKPYHKFMAFKSFADLPHRPLLVDLTVEEGQR LKVIYGSSAGFHAVDVDSGNSYDIYIPVHIQSQIT PHAIIFLPNTDGMEMLLCYEDEGVYVNTYGRJIK DVLQWGEPMPTSVAYICSNQIMGWGEKAIEIRS VETGHLDDGVFMHKRAQRLKFLCERNDKVFFASV RSGSSQVYFMTLNRNCIMNW
3784	A	1213	457	LSPRQVDGLAGLQKGLSLSLLYQFLMNGIRLGT GLAEAGGYLHTAEGTHSPARSAAGAMAGVMG AYLGSPIMVKTHLQAQAASEIAVGHQYKHQG MFQALTEIGQKHGLVGLWRGALGGLPRVIVGSS TQLCTFSSTKDLLSQWEIFPPQSWKLALVAAMM SGIAVVLAMAPFDVACTRLYNQPHRCTGQGPVLY RGILDALLQTARTEGIFGMYKGIGASYFRLGPHTI LSLFFWDQLRSLYYTDTK
3785	A	193	813	RRRGRHSLCGGKMLAYCVQDATVVDVEKRRNP SKHYVYIINVTWSDSTSQTYYRY\SKFFDLQMQ LD\KFPINESGQKDPKQRIIPFLPGKILFRSHIRDV AVKRLKPIDEYCRALVRLPPHISQCDEVFRFFEAR PEDVNPPKEQGSPDDAVLPYGVNKGKQELKAG PNWPGRTHHVNCVTQKCLFVFHFKFSSSGNKE SKSL
3786	A	3785	1632	EFVGRAASTTVVTRIAWRMADAGIRRVVPSDLY PLVLGFLRDNLSEVANKFAKATGATQQDANAS SLLDIYSFWLNRSAKVPERKLQANGPVAKKAKK KASSSDSEDSSEEEEEVQGPPAKKAAVPAKRVL PPGKAAAKASESSSSSESSDDDEEDQKKQPV KGVPQAKAGQAPPKKAASSDSDSDSSEDEPP KNQKPKITPVTVKAQTKAPPKPARA\APKIANGK AASSSSSSSSSSDDSEEEKAAATPKKTPKKQV VAKAPVKAATTPTRKSSSSSEDSSDEEEQKKPM KNKPGPYSSVPPSAPPPKSLGTQPPKAVEKQ QPVESSEDSSDESDDSSSEEEKPPTKAVVSKATT PPPAKKAESSDSSDSDSSEDEDEAPSKPAGTTK NSSNKPAVTTKSPA VKPAAAPKQPVGGGQKLLT RKADSSSSEESSSEEEKTKKMAVATTKPKATAK AALS LPAKQAPQGSRDSSSDSDSSSSEEEEEKTSK SAVKKKPKQVAGGAAPSKPASAKKGKAESSNSS SSDSSSEEEEEKLKKGSPRPQAPKANGTALTA QNGKAAKNSEEEEEKKAAVVVSKSGSLKKR KQNEAAKEAETPQAKKIKLQTPNTFPKRKKGEK RASSPFRRVREEIEVDSRVADNSFDAKRGAGD WGERANQVLKFTKGKSFHEKTKKRGSGSYRG SISVQVNSIKFDSE
3787	A	3	5078	IPEG/RALSAEHTSSLVPSLHITLQGQEQAILSGAV PASPSTGTADFPSILTFLQPTENHASPSVPPEMPTL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				<p>PAEGSDGSPPATRDLLSSKVPNLLSTSWTFPRW KKDSVTAILGKNEEANVTIPLQAFPRKEVLSLHT VNGFVSDFSTGSSVSPITAPRTNPLPSGPPLPSILS IQATQTVFPSELLAFSSTKPEVYAAAVDHSGLPAS APKQVRASPSSMDVYDSLITGDMKKPATTDVFW SSLSAETGSLSTESIISGLQQQTNYDLNGHTISTTS WETHLAPTAPPNGLTSAADAISQDFKDTAGHS VTAEGFSIQDLVLGTSIEQPVQQSDMTMVGSHID LWPTSNNNHSRDFQTAEVAYYSPTTRHSVSHQP LQLPNQPAHPLLLTSPGPTSTGSLQEMLSDGTD GSEISSDINSSPERNASTPFQNILGYHSAEASSISTS VFPRTSRVLRSQHPKKTADTVSSKVQPTAA AAVTLFLRKSSPPALSAALVAKGTSSSPLAVASG PAKSSMTTLAKNVTNKAASGPKRTPGAVHTAF PFTPTYMYARTGHTTSTHTA/IARKHGHCLWPVV YNLP/PP/GKPQAMHTGLPNPTNLEMPRASTPRPL TVTAALTSITASVKAIRLPLRAENTDAVLPAAS AAVVTGKMASNLECOMSSKLLVKTVLFLTQRR VQISESLKFSIAKGLTQALRKAFHQNDVSAHVDI LEYSHNVTVGYYATKGLVYLPVAVIEMLGVI GVSNVTADLKQHTPHLQSVAVLASPWNQPGAG YFQLKTVLQFVSQADNIQSCKFAQTMEQRLQKA FQDAERKVLNTKSNLTQIVSTSNASQAVTLVYV VGNQSTFLNGTVASSLLSQLSAELVGFYLYTPPL TIAEPLEYPNLDISETTRDYWVITVLQGVDSL GLHNQSFARVMEQRLAQLFMMSQQQGRFRKRA TTLGSYTVQMVKMQRVPGPKDPAELTYTYLYN GKPLLGTAAAKILSTIDSQRMALTLHHVLLQAD PVVKNPPNNLWIIAAVLAPIAVVTVIIIITAVLCR KNKNDFKPDMTINLPQRAKPVQGFYAKQHLG QQGADEEVIPVTQETVVLPLPIRDAPQERDVAQD GSTIKTAKSTETRKSRSPSENGSVISNESGKPSGR RSPQNVMAQQKVTKKEARKRNVPADEEEGAV LFDNSSKVAAPFDTSSGSVQLIAIKPTALPMVPP TSDRSQESSAVLNGEVNKALKQKSDIEHYRNKL RLKAKRKGYYDFPAVETSKGLTERKKMYEKAP KEMEHVLDPDSELCAFTESKNRQMKNSVYRS RQSLNSPSPGETEMDLLVTRERPRRGIRNSGYDT EPEIIEETNIDRVPEPRGYSRQVKGHSETSLSS QPSIDEVRQQMHMLLEEAFSLASAGHAGQSRHQ EAYGSAQHLPYSEVVTAPGTMTRPRAGVQWVP TYRPEMYQYSLPRPAYRFSQLPEMVMGSPPPVP PRTGPVAVASLRRSTSDIGSKTRMAESTGPEPAQ LHDSASFTQMSRGVSVTQLDQSALNYSNTVP AVFAIPAANRPGFTGYFIPTPPSSYRNQAWMSYA GENELPSQWADSVPLPGYIEAYPRSRYPQSSPSRL PRQYSQPANLHPSLEQAPAPSTAASQQSLAENDP SDAPLTNISTAALVKAIREEVAKLAKKQTDMEF QV</p>
3788	A	2	1737	<p>MKGLYTDAMKSDNVKDKDAKISFLQKAIDVV VMVSGEPLAKPARIVAGHEPERTNELLQIGKC CLNKLSSDDAVRRVLAGEKGEVKGRASLTSRSQ ELDNKNVREEESRVHKNTEDRGDAEIKERSTSRD RKQKEELKEDRMPREKDKDKEKAKENGGNRHR EGERERAKARAPDNERQKDRGNRERDRDSERK</p>

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KETERKSEGGKEKERLRDRDRERDRDKGKDRDR RRVKNGEHSWDLDRENNREHDKPEKKSASSGE MSKKLSDGTFKDSKAETETETISTRASKSLTTKTS KRRSKNSVEGDSTSDAEGDAGPAGQDKSEVPET PEIPNELSSNIRRIIPRPGSARPAPPRVKRQDSMEAL QMDRSGSGKTVSNVITESHNSDNEEDDQFVVEA APQLSEMSEIEMVTAVELEEEKHGGLVKKILET KKDYEKLQQSPKPGEKERSLFESAWKKEKDIVS KEIEKLRTSIQTLCKSALPLGKIMDYIQEDVDAM QNELQMYHSENHQHAEALQQEQRITDCAVEPL KAELA\ELEQLIKD\Q/QDKICAVKANILKNEEKIQ KMOVSYNLTSSR
3789	A	1	4369	MRTLGTCLATLAGLLLTAAGETTSGGCLFDEPYS TCGYSQSEGDDFNWEQVNTLTPTSDPWPMPGS FMLVNASGRPEGQRAHLLLPQLKENDTHCIDFH YFVSSKSNPPGLLNVYVKVNNGPLGNPIWNISG DPTRTNRAELAISTFWPNFYQVIFEVITSGHQG YLAIDEVKVLGHPCTRTPHFLRIQNVNAGQFA TFQCSAIGRTVAGDRLWLQGDVVRDAPLKEIKVT SSRRFIASFNVVNTTKRDAGKYRCMIRTEGGVGI SNYAEVVKPPVPIAPPQLASVGATYLVWLQNL ANSINGDGPVAREVEYCTASGSWNRQPVDS YKIGHLDPDTEYEISVLLTRPGEGGTGSPGALRT RTKCADPMRGPRKLEVVEVKSQRQITIRWEPFGY NVTRCHSYNLTVHYCYQVGGQEQVREEVSWDT ENSHPQHTITNLSPTYTNVSVKLILMNPEGRKESQ ELIVQTDDELPGA VPTESIQQSTFEKIFLQWREP TQTYGVITLYEITYKAVSSFDPEIDLSNQSGRVSK LGNETHFLFFGLYPGTTYSTIRASTAKGFGPPAT NQFTTKISAPSMPIAYELETPLNQTDNTVTVMLKP AHSRGAPVSVYQIVVEEERPRRTKKTTTEILKCYP VPIHFQNASLLNSQYYFAAEFPADSLQAAQPFTIG DNKTYNGYWNTPLLPYKSYRIYFQAASRANGET KIDCVQVATKGAATPKPVPEPEKQTDHTVKIAG VIAGILLFVIFLGVVLMKKRKLAKKRKETMSS TRQEIDLWIGELNGPRSYAEQGTKLATRAFSMD THNLNGRSVSSPSFTMKTNLTSTSPNSYYPDE THTMASDTSSLVQSHTYKKREPADVYPYQTGQLH PAIRVADLLQHITQMKCAEGYGFKEEYESFFEGQ SAPWDSAKKDENRMKNRYGNIIAYDHSRVRQLT IEGDTNSDYINGNYIDGYHRPNHYIATQGPMQET IYDFWRMVWHENTASIIMVTNLVEVGRVKCK YWPDDTEIYKDIKVTLIETELLA EYVIRTFAVEKR GVHEIREIRQFHFTGWPDHGVPHYATGLLGFVR QVKSXSPPSAGPLVVHCSAGAGRTGCFIVIDIML DMAEREGVVDIYNCVRELRSRRVNMVQTEEQY VFIHDAILEACLCGDTSPASQVRSLYYDMNKLD PQTNSSQIKEEFRTLNMVPTLRVEDCSIALPRN HEKNRCMDILPPDRCLPFLITIDGESSNYINAALM DSYKQPSAFIVTQHPLPNTVKDFWRLVLDYHCTS VVMLNDVDPAQLCPQYWPENGVHRHGPIQVEF VSADLEEDIISRIFRIYNAARPQDGYRMVQQQFQL GWPMYRDTVPVSKRSFLKLIRQVDKWQEEYNGG EGRTVVHCLNGGGRSGTFCAISIVCEMLRHQRTV DVFHAVKTLRNNKPNMVDLLDQYKFCYEVALE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3790	A	261	485	YLNSG EEQTPLHIASRLGKTEIVQLLLQHMAHPDAATTN GYTPLHISAREGQV\DV\ASVLLGRQGAHFSRLT KVRRMTS
3791	A	1	5874	LPPVTMSGKYIMEEHDSYSDQVWSIDELPSKQG YYLQGNYLRCVAEVGSFEHNLTTDLLNHLVVFQ KVFMKEVNEVIQKVSGGEQPIPLWNEHDGTADG DKPKILLYSLNLQFKGIQVTATTPSMRAVRFETG LIELELSNRLQTKASPGSSSYLKLFGKCQVDLNL ALGQIVKHQVYEEAGSDFHQVAYFKTRIGLRNA LREEISGSSDREAVLITLNRPIVYAQPVAFDRAVL FWLNYKIAAYDNWNEQRMALHKDIHMATKEVV DMLPGIQQTSAQAFGTPFLQLTVNDLGICLPITNT AQSNHTGDLDTGSAVLVTIESTLITACSSSELVSK GHFKNFCIRFADGFETSWDDWKPEIHGDLVMNA CVVPDGTYEVCSTTGQAAAESSSAGTWTLNVL WKMCGIDVHMDPNIGKRLNALGNTLTTLTGEED IDDIADLNSVNIADLSDEDEVDTMSPTIHTTEADTY RRQAASASQPGELRGRKIMKRIVDIRELNEQAKV IDDLKKLGASEGTINQEIQRYQQLESVAVNDIR DVRKKLRSSMRAASLKDKWGLSYKPSYSRSKS ISASGRPPLKRMERASSRVGETEELPEIRVDAASP GPRVTFNIQDTFPEETELDLLSVTIEGPSHYSSNSE GSCSVFSSPKTPGGFSPGIPFQTEEGRRDLSSTS EDSEKDEKDEHERERFYIRKPSHTSRKKA TGF AAVHQLFTERWPTTPVNRSLSGTATERNIDFELD IRVEIDSGKCVLHPTTLLQEHDDISLRRSYDRSSR SLDQDSPSKKKKFQNTYASTTHLMTGKKVPSSL QTKPSDLETTVFYIPGVDVKLHYNKTLKTESPN ASRGSSLPRTLSKESKLYGMKDSATSPSPPLPST VQSKTNTLLPPQPPPIPAAKGKGSGGVKTAKLYA WVALQSLPEEMVISPCLLDFLEKALETIPITPVER NYTAVSSQDEDMGHFEIPDPMEES\TSLVS\SSTS AYSSFPVDVVVYVRVQPSQIKFSCLPVSRVECML KLPSLDLVFSSNRGELETGTTPAETLSPGGNA TQSGTKTSASKTGIPGSSGLGSPGRSRHSSSQSD LTSSSSSSSGLSFTACMSDFSLYVFHPYGAGKQIT AVSGLTPGSGGLGNVDEEPTSVTGRKDSL SINLE FVKVSLSRIRSGGASFFESQSVSKSASKMDTTLI NISAVCDIGSASFYDMRRLSEILAFPRAWYRRSI ARRLFLGDQTINLPTSGPGTPDSIEGVSQHLSPSS RKAYCKTWEQPSQSASFTHMPQSPNVFNEHMTN STMSPGTVGQSLKSPASIRSRVSDSSVPRRDSLS KTSTPFNKSNKAASQQTGWETLVVFAINLKQL NVQMNMNSVMGNTTWTSSGLKSQGRLSVGSNR DREISMSVGLGRSQLDSKGGVVGGTIDVNALEM VAHISEHPNQPSHKIQTMGSTEARDVYMGSSIL MGIFSNADLKLQDEWKVNL YNTLDSSITDKSEIF VHGDLKWDIFQVMISRSTTPDLIKIGMKLQEFFT QQFDTSKRALSTWGPVYLPKMTSNLEKSSQE QLLDAAHHRHWPGVLKVVSCHISLFQIPLPEDG MQFGGMSLHGNHMTLACFHGPNFRSKSWALF HLEEPNIAFWTEAQKIWEDGSSDHSTYIVQTLDF HLGHNTMVTKPCGALESPMATITKJITRRRHNPP HGVASVKEWFNYVTATRNEELNLLRNVDANNT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ENSTTVKNSSLLSGFRGGSSYNHETETIFALPRM QLDFKSIHVQEPQEPSLQDASLKPKVECSVVTEF TDHICVTMDAELIMFLHDLVSAYLKEKEKAIFPP RILSTRPGQKSPIIHDDNSSDKDREDSITYTTVDW RDFMCNTWHLEPTLRLLISWTGRKIDPVGVDYILQ KLGFFHHARTTIPKWLQRGVMDPLDKVLSVLKK LGTALQDEKEKKGKDKEEH
3792	A	1	364	QNGSTPLHHAASKNRHEIALMLLEGGANPDGKD HYEATAKHQATAKGNFKMIHILLYKASTIIQDT EGNTPPHLVCDRVEEAKLLVSQGA/SIYIENKEE KDP/LQVAKGALGLVLKRMVEG
3793	A	2	340	DIVPNPKMAPLGDEAPTLEKVLTPELSEEEVSTR DDIQFHHFSSEEALQKVYFVAKEDPSSQEEAHT PEAPPPQPPSSERCLGEMKCTLVRGDSSPRQAE KSGPASRPAL
3794	A	421	158	SYWVGEDYTYKFFEVLIDPFHKAIRRNPDQTWI SKAVYKHREMCGLTSTGRKSHGLEKDRMFPHAI GGSCRAA*RRRKTLLQFPCYH
3795	A	24	592	GGMDSRVSGTTSNGETKPVYPVMEKKEEDGTLE RGHWNNKMEFVLSVAGEIIGLGNVWRFPYLCYK NGGGAFFIPYLVFLFTCGIPVFLLETALGQYTSQ GVTAWRKICPIFEGIGYASQMIVILLNVYIIVLA WALFYLFSSFTIDLPGWGGCYHEWNTHECMEFQK TNGSLNGTSENATSPVIEFW
3796	A	3	592	KPASTYSTSQPSMAPLLPIRTLPILILLALLSPGA ADFNISLSSGLLSPALTESLLVALPPCHLTGGNAT LMVRRANDSKVVTSSFVPPCRGRRELVSVDSD GAGFTVTRL SAYQVTNLVPGTKFYISYLVKKG ATESSREIPMFTLPRRNMESIGLMARTGGMVVI TVLLSVAMFLLVLGFIALALGSRK
3797	A	1	1556	ATRLRGSGSWGCSRLRFGPPAYRRFSSGGAYPN IPLSSPLPGVPKPVFATVDGQEKFTKVTTLNGL RVASQNKFGQFCTVGILNSGSRYEAKYLSGIAH FLEKLAFSSTARFDSKDEILLLEKHGGICDCQTS RDTTMYAVSADSKGLDVTVALADVVLQPRLT DEEVEMTRMAVQFELEDNLNRPDPEPLLEMIHE AAYRENTVGLHRCPTENVAKINREVLHLSYLRN YYTPDRMVLAVGVGEHEHLVDCARKYLLGVQP AWGSAEAVDIDRSVAQYTGGAJLERDMSNVSL GPTPIPELTHIMVGLESCSFLEEDFIPFAVLNMMM GGGGSFSAGGPGKGMFSRLYLNVLNRHHWMYN ATSYHHSYEDTGLLCIHASADPRQVREMVEIITK EFILMGGTVDTVELERAQTQLTSMMLMNLESRP VIFEDVGRQVLATRSRKLPHLCTLRNVKPEDV KRVASKMLRGKPAVAALGDLTDLPTYEHIQTAL SSKDGRLPRTYRLFR
3798	A	73	759	KRLVEAGVPRTFDGIVGEGGAQSRSCWPWGVTA QTPAFSADSLNCLKNCMSITMGSVRPSVEQFHKY LPWFLNDRPNIKCPKGGLAAYSTSVNLTSQGQV LASRFMAYHKPLKNSQDYTEALRAARELANIT ADLRKVPGTDPAFEVFPYITINVFYEQYL TILPEG LFMLSLCLVPTFAVSCLLGLDLRSGLLNLLSIV MILVDTVGFMALWGISYNAVSLINLVS
3799	A	73	759	KRLVEAGVPRTFDGIVGEGGAQSRSCWPWGVTA QTPAFSADSLNCLKNCMSITMGSVRPSVEQFHKY

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LPWFLNDRPNIKCPKGGLAAYSTSVNLTSDGQV LASRFMAYHKPLKNSQDYTEALRAARELAANIT ADLRKVPGTDPAFEVFPYITNVFYEQYL TILPEG LFMLS LCLVPTFAVSCLLLGLDLRSGLLNLLSIV MILVDTVGFMALWGISYNAVSLINLVS
3800	A	250	1032	GIFRSLRVLFPLFSVGRPQFARSLSAAPQLSDTAD TMGFGDLKSPAGLQVLNDYLADKSYIEGYVPSQ ADVAVFEAVSSPPADLCHALRWYNHIKSYEKE KASLPGVKKALGKYGPADVEDTTGSGATDSKD DDDIDLFGSDDEEESEEAKRLREERLAQYESKKA KKPALVAKSSILLDVKPWDDETDMAKLEECVRS IQADGLVWGSSKLVPGYGIKKLQIQCVVEDDK VGTDMLEEQITAFEDYVQSMMDVAAFNKI
3801	A	155	656	SREMELVTRFDVAIEFSPPEWKCLDPAQQNL YR DVMLENYRNLVSLGFVISNPDLVTCLEQIKEPCN LKIHETAAPPAICSPFSQDLSPVQGIEDSFHKLIL KRYEKC GHENLQLRGCKRVNECKVQKGVNNG VYQCLSTTQSKIFQCNTCVRVFTSSHSNKHK
3802	A	1	1428	VTVSPETHMDLTKGCVTFEDIAIYFSQDEWGLLD EAQRLLYLEVMLENFALVASLGC GHGTEDEETP SDQNVSVGVSSQSKAGSSTQKTQSCMCVPVLKD ILHLADLPGQKPYLVGECTNHHQHOKHHS AKKS LKRDMDRASYVKCCLFCMSLKPFRKWEV GKDL PAMLRLLRSLVFPGGKKPGTITECGEDIRSQKSH YKSGECGKASRHKHTPVYHPRVYTGKKLYECSK CGKA FRGKYSLVQHQRVHTGERPWECNECGKF FSQTSHLNDHRRHTGERPYECSECGKLFRQNSS LVDHQKIHTGARPYECSQCGKSFSQKATLVKHQ RVHTGERPYKCGECGNSFSQSAILNQHRRHTGA KPYECGQCGKSFSQKATLIKHQRVHTGERPYKC GDCGKSFSQSSILIQHRRHTGARPYECGQCGKSF SQKSGLIQHQQVVHTGERPYECNKGNSFSQCSSL IHHQKCHNT
3803	A	193	617	LFPFLGSESKNGEADSSDKEMKHGQKSPTGKQTS QHLKRLKKSGLGHLKWTKAEDIDIEPTGSILVNT NLRALINKHTFASLPQHFQQYLLLLLPEVDRMG SDGILRLSTSALNNEFFAYAAQGWKQRLAEGKF VFSIIM
3804	A	197	479	SSSRASPPEHPSSQAHCGLVLSHACPEVTNKWS TGSSSSPNSSWVSSPLQPEGLSGSSRMKGGSATKI LLETLLAAHMTADQGIASSQRCLL
3805	A	1	385	QSADTLFPGDINFNVSGLFSAVTLQDTVSDRLAS EELPSTAVPTPATTPAPAPAPATAPALVSAAT KERTSEVPPRPASPKVTRSPPETAAPVEDMARR SELA VGGEEGTEGGRGEGTGSPMSSY
3806	A	47	1033	LQGD TWHL SFLSHFSRLHGGVPGRGLLEGNNLQ PQAPGHDMTSIPFPGDRLLQVDGVILCGLTHKQA VQCLKGPGQVARLV LERRVPRSTQQCPSANDSM GDERTAVSLVTALPGRPSSCSVSTDGPKF*SSN* KRIANGLGFSFVQMEKESCSHLKSDLVRIKRLFP GHPAEENGAIAGDIILGREWEGPRKASSSRCRG SWAMQLSVQAGPSFASYYPAAVEVLHLLRGAPQ EVTLLLCRPPPGALPELEQEWQTPELSADKEFTR ATCTDSCTSPILGSRGQLGGTVPPQMKGKA WGL RPESQKAIREGTMGAKTERDLGPVP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3807	A	656	1238	RCPSLLPPSWPLPTLQTLTRTPGNKAIAGGAGLW AVLWGSERTPPYR*GN*NQRGA VPCLRPHRLRP QDKFLVLASDGLWDMLSNEDVVRLVVGHLEAE DWHKTDLAQR PANLGLMQSLLLQRKASGLHEA DQNAATRLIRHAIGNNEY GEMEAERLAAMLTLF EDLARMYRDDITVTVVYFNSESIGAYYKGG
3808	A	26	2195	SQYSESVAGRQASPERLLGSYHAMASTVEGGDT ALLPEFPRGPLDAYRARSFSWKELALFTEGEG MLRFKKTIFSALENDPLFARSPGADLSLEKYREL NFLRCKRIFEYDFLSVEDMFKSPLKVPALIQCLG MYDSSLAACKYLLHSLVFGSAVYSSGSRHLTYIQ KIFRMEIFGCFALTELSHG SNTKAIRTTAHYDPAT EEFIHSPDFEAAKFVWGNMGKTATHAVVFAKL CVPGDQCHGLHPFIVQIRDPKTLMPMPGVMVGDI GKKLQGQNGLDNGFAMFHKVRVPRQSLLNRMGD VTPEGTYVSPFKDVRQRF GASLGSLSGRVSIVSL AILNLKLAVAIALRFSATRRQFGPTEEEIPVLEY PMQQWRLLPYLA AVYALDHFSKSLFLDLVELQR GLASGDRSARQAE LGREIHALASASKPLASWTT QQGIQECREACGGHGYLAMNRLGVLRDDNDPN CTYEGDNNILLQQTSNYLLGLLAHQVHDGACFR SPLKSVDFLDAYPGILDQKFEVSSVADCLDSA VA LAAYKWLV CYLLRETYQKLNQEKRS GSSDFEAR NKCQVSHGRPLALAFVELTVVQRFHEHVHQPVS PPSLRAVLGRLSALYALWSLSRHAALLYRGGYF SGEQAGEVLES AVLALCSQLKDDA VALVDVIAP PDFVLDSPIGRADGELYKNLWGAVLQESKVLER ASWWPEFSV NKPVIGSLKSKL
3809	A	117	830	CFGIMERVGCTLT TTYAHPRPTNFLPAISTMAS SYRDRFPHSNLTHSLPWRPSTYYKVASNSPSV APYCTRSQRVSENTMLPFVSNRTTFFTRYTPDDW YRNL TNYQESNTSRHNSKLRVDTSRLIQDKYQ QTRKTQADTTQNLGERVNDIGFWKSEIHELD IGETNALTDVKKRLERALMETEAPLQVARECLF HREKRMGIDL VHDEVEAQLTVNVGEMHQSQA A
3810	A	3	518	VIQLEGGSGADLGEHSCR PASQPRFPRPAEARS HPATRRPASGPAMGKTNSKLAPEVLEDLVQNT FSEQLKQWYKGFLKDCPSGILNLEEFQQLYKF FPYGDASKFAQHAFRTFDKNGDGTIDFREFICAL SVTSRGSFEQKLNWAFEMYDL DGDGRITRLEML EIIIE
3811	A	81	1147	GCGYGCSGAGGAAIGEPMAK WGE GDRWVIVEE RADATNVNNWHWTERDASNWSTD KLTFLAV QVQNEEGKCEVTEVSKLDGEASINNRKGKLIFFY EWSVKLNWTGTSKSGVQYKGHVEIPNLSSENSV DEVEISVSLAKDEPD TNLVALMKEEGVKLLREA MGIYISTLKTEFTQGMILPTMNGESVDPVGPAL KTEERKAKPAPSKTQARPVG VKIPTCKITLKETFL TSPEELYRVFTTQELVQAFTHAPATLEADRG GKF HMDVGNVSGEFTDLVPEKHVMKWRFKSWPEG HFATITLTFIDKNGETELCMEGRGIPAPEERTRQ GWQRY YFEGIKQTFGYGARLF
3812	A	20	558	PCGTAASTHAYDRRAKCRQQQQQQQNGGQNKV RPAKKKTSPAREVSSSESGTSGQFTPPSSTSVPTIAS

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SSAPVSIWSPASISPLSDPLSTSSSCMQRSYPMTYT QASGYSQGYAGSTSYFGGMDCGSYLTPMHHL PGPGATLSPMGNTNAVTSHLNQSPASLSTQGYGAS KLWGFNFNH
3813	A	1	1016	CTEPPRRSTRTPAALASLRPYTDYVVVSDQILQES EDFFTLIESHEGKPLKLMVYNSKSDSCREVTVP NAAWGGEGSLGCGIGYGYLHRIPTQPPSYHKKPP GTPPPSALPLGAPPPDALPPGPTPEDSPSLETGSRQ SDYMEALLQAPGSSMEDPLPGPGSPSHSAPDPDG LPHFMETPLQPPPPVQRVMDPGFLDVSGISLLDN SNASVWPSLPSSTELTTAVSTSGPEDICSSSSSHE RGGEATWSGSEFEVSFLDSPGAQAQADILPLQLT LPDSL TSAASPEDGLSAELLEAQAEPEPASTEGLD TGTEAEGLDLSQAQISTTE*HPGL*QGP
3814	A	2	884	VFWQVRNAGSSPLSAACPLFRTPAPQPCGSWGR CCIPHASTGCRPMAERGELDTGAKQNTGVWL KVPKYLSSQWAKASGRGEVGLRLAKTQGRTE VSFTLNEDLANIHDIGGKPASVSAPREHPFVLQSV GGQTLTVFTSSSDKLSLEGIVVQRAECRPAASE NYMRLKRLQIEESSKPVRLSQQLDKVVTNYKP VANHQYNIEYERKKKEDGKRARADKQHVLDML FSAFEKHQYYNLKDLDITKQPVVYLKEILKEIG VQNVKGIHKNTWELKPEYRHYQGEEKSD
3815	A	17	411	NIGDWEDIGKSPERIIQYYGPATWAQDGSRGYCT PIYMLNHIIRLQAVLEIIMNERANALDLLAQOTTK MRNANYQNRLALDYLLAHEGGV*GKFSLTNCC LEIDDNGKAIMEITARMRKL AHIPVQTWER
3816	A	3	1172	SHWQRRDRRCVRNMAERGRKPCGPGEHGQRI EWRKWKQKKKEKKKKWKDLKLMKKLERQRAQ EEQAKRLEEEEA AAEKEDRGRPYTL SVALPGSIL DNAQSPELRTYLAGQIARACAIFCVD EIVVFDEE GQDAKTVEGEFTGVGKKGQACVQLARILQYLEC PQYLRKAFFPKHQDLQFAGLLNPLDSPHMRQD EESFREGVVVDRPTRPGHGSFVNCGMKKEVKI DKNLEPLRLVTVRLNQQQHPDCKTYHGKVVSS QDPRTKAGLYWGYTVRLASCLSAVFAEAPFDG YDLTIGTSERGSDVASAQLPNFRHALVVFGLQG LEAGADADPNLEVAEPSVLFDLVNTCPGQGSR TIRTEAILISLAALQPLIQAGARHT
3817	A	246	1197	FLSAGMSNFTHYAYLLMIESLMLGKVPHPVPSH HFIFHDDGSARQKGESDYKVIIQQWFSKSGPWT SSNVTWGLLELQQSISESAVLTIPPGDSGAGSNLI TMFLNRNKETDLCGRSKVNRGWNSGRCKQRG KTEQPGEPLHVYVTIKHA VALESRHQKGELQC LIKMCIPLSKPLQMFFSPPHWEA WLQRVQQLAK NTRYFRQRLQEMGFIIYGNENASVVP LLLYMPG KVAAFARHMLEKKIGVVVVGFPATPLAEARARF CVSAAHTREMLD TVLEALDEMGDLLQLKYSRH KKSARPELYDETSFELED
3818	A	215	789	NPQSSSSEGSSEIFQVNGHNRLLVQRSEVTQAPG QYTVDVEGHGCTFIQATLKYNVLLPKKASGFSLS LEIVKNYSSTAFDLTVTLKYTGIRNKSSMVIDV KMLSGFTPTMSSIELENKGQVMKTEVKNDHVL FYLENVFGRA DSFTFSVEQSNLVFNIQAPGMVY DYYEKEEYALAFYHINSSSVSE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3819	A	1	1483	RIPDSIISRGVQGLPRDTASLSTTPSESPRAQATSR LSTASCPTPKVQSRCSSKENILRASHSAVDITKVA RRHRMSPFPLTSMDFKAFITVLEMPVLGTEIINYR DGMGRVLAQDVYAKDNLPPFPASVKDGYAVRA ADGPGDRFIIGESQAGEQPTQTVMPGQVMRVTT GAPIPCGADAVVQVEDTELIRESDDGTEELVRIL VQARPGQDIRPIGHDIKRGECVLAKGTHMGPSIEI GLLATVGVTEVEVNKFPVAVMSTGNELLNPED DLLPGKIRDSNRSTLLATIQEHGYPTINLGIVGDN PDDLLNALNEGISRADVITSGGVSMGEKDYLKQ VLDIDLHAQIHFGVRVFMKPGPLPTTFATLDDIGVR KIIFALPGNPVSAVVTCNLFVVPALRKMQGILDP RPTIIKARLSCDVKLDPRPEYHRCILTWHHQEPLP WAQSTGNQMSSRLMSMRANGLMLPPKTEQY VELHKGEVVDVMVIGRL
3820	A	2216	487	PQEPALKSEFSQVASNTIPLPLPQNTCKDNGPCK QVCSTVGGSALCSFCPGYAIMADGVSCEDQDECL MGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYI LNAHRKCVDINECVTDLHTCSRGEHCNVTLGSF HCYKALTCEPGYALKDGECEVDDECAMGTHTC QPGFLCQNTKGSFYCQARQRCMDGFLQDPEGNC VDINECTSLSEPCRPFGFSCINTVGSYTCQRNPLIC ARGYHASDDGTKCVDVNECETGVHRCGEGQVC HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWAS PGRLCQHTCENTLGSYRCSGASGFLAADGKRC EDVNECEAQRCSQECANIYGSYQCYCRQGYQLA EDGHTCTDIDECAQGAGILCTFRCLNVPGSYQCA CPEQGYTMTANGRSCKDVDECALGTHNCSEAET CHNIQGSFRCLRFECPPNYVQVSKTKCERTTCHD FLEQNSPARITHYQLNFQTGLLVPAHIFRIGPAP AFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYL QRAVLEPRDFALDDEMKLWRQGSVTTFLAKMHI FFTTFAL
3821	A	2216	487	PQEPALKSEFSQVASNTIPLPLPQNTCKDNGPCK QVCSTVGGSALCSFCPGYAIMADGVSCEDQDECL MGAHDCSRRQFCVNTLGSFYCVNHTVLCADGYI LNAHRKCVDINECVTDLHTCSRGEHCNVTLGSF HCYKALTCEPGYALKDGECEVDDECAMGTHTC QPGFLCQNTKGSFYCQARQRCMDGFLQDPEGNC VDINECTSLSEPCRPFGFSCINTVGSYTCQRNPLIC ARGYHASDDGTKCVDVNECETGVHRCGEGQVC HNLPGSYRCDCKAGFQRDAFGRGCIDVNECWAS PGRLCQHTCENTLGSYRCSGASGFLAADGKRC EDVNECEAQRCSQECANIYGSYQCYCRQGYQLA EDGHTCTDIDECAQGAGILCTFRCLNVPGSYQCA CPEQGYTMTANGRSCKDVDECALGTHNCSEAET CHNIQGSFRCLRFECPPNYVQVSKTKCERTTCHD FLEQNSPARITHYQLNFQTGLLVPAHIFRIGPAP AFTGDTIALNIIKGNEEGYFGTRRLNAYTGVVYL QRAVLEPRDFALDDEMKLWRQGSVTTFLAKMHI FFTTFAL
3822	A	2502	1540	MAAATRGCRPWGSLGLGLVSAAAAAWDLAS LRCTLGAFCECDFRPDLPGLECDLAQHLAQHL AKALVVKALKAFVRDPAPTKPLVLSLHGWTGTG KSYVSSLLAHYLFQGGRLSPRVHHFSPVLHFPHP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SHIERYKKDLKSWVQGNLTACGRSLFLFDEMDK MPPGLMEVLRPFLGSSWVYGTNYRKAIFIFISN TGGEQINQVALEAWRSRRDREEILLQELEPVISR AVLDNPHHGFSSNGIMEERLLDAVVPFLPLQRHH VRHCVLNELAQLGLEPRDEVVQAVLDSTTFPE DEQLFSSNGCKTVASRIAFFL
3823	A	1	3174	YGCEKTTEGRIPLKNYRLFSADRKRVETALEAC SLPSSRNDSIPQEDFTPEVYRVFLNNLCPRPEIDNI FSEFGAKSKPYLTVQMMDFINLKQRDPRLNEIL YPPLKQEQVQVLEIKYEPNNSLARKGQISVDGFM RYLSGEENGVSPEKLDLNEEDMSQPLSHYFINSS HNTYLTAGQLAGNSSVEMYRQVLLSGCRCVELD CWKGRTAEEEPVITHGFTMTTEISFKEVIEAIAEC AFKTSPPFILLSFENHVDSPKQQAQMAEYCRLIFG DALLMEPLEKYPLESGVPLPSPMDLMYKILVKN KKKSHKSSESGSGKKKLEQASNTYSDSSSMFEP SPGAGEADTESDDDDDDDDCKKSSMDEGTAGSE AMATEEMSNLVNYIQPVKFESFEISKRNKSFEM SSFVETKGLEQLTKSPVEFVEYNKMQLSRIYPKG TRVDSSNYMPQLFWNAGCMVALNFQTMDLA MQINMGMYEYNGKSGYRLKPEFMRRPDKHFD FTEGIVDGIVANTLSVKIISGQFLSDKKVGTYVEV DMFGLPVDTRRKAFKTKTSQGNVNPVWEEPI VFKKVVLPTLACLRIAVYEEGGKFIGHRILPVQAI RPGYHYICLRNERNQPLTLPAVFVYIEVKDYVPD TYADVIEALSNPIRYVNLMEQRAKQLAALTLEDE EEVKKEADPGETPSEAPSEARTTPAENGVNHTTT LTPKPPSQALHSQPAPGSVKAPAKTEDLIQSVLTE VEAQTIEELKQKSFVKLQKKHYKEMKDLVKR HHKKTDLIKEHTTKYNEIQNDYLRRAALEKS AKKDSKKKSEPSSPDHGSSTIEQDLAALDAEMTQ KLIDLKDKQQQQLNLNRQEQYYSEKYQKREHIK LLIQKLTDAEBCQNNQLKKLKEICEKEKELKK KMDKKRQEKITEAKSKDKSQMEEEKTEMIRSYI QEVVQYIKRLEEAQSKRQEKLEKHKEIRQQILD EKPKLQVELEQEQYQDKFKRLPLEILEFVQEAMKG KISEDNSHGSAPLSLSSDPGKVNHKTPSSEELGGD IPGKEFDTP
3824	A	1	426	ILHWFVHRWSGRNNREKIGVHVGFEEILNMEPY CCRETLKSLRPECFIYDLSAVVMHHGKGFGSGH YTAYCYNSEGGFWVHCNDSKLSMCTMDEVCKA QAYILFYTQRVTENGHSLKLLPELLLSGQHPNED ADTSSNEILS
3825	A	3	364	GIRAKFPNKIPVVVERYPRETFLPPLDKTKFLVPQ ELTMTQFLSIHRSMVLRATEAFYLLVNNKSLVS MSATMAEYRDYKDEDGFVYMTYASQETFGCLE SAAPRDGSSLEDRLHPL
3826	A	1	1237	PEKKFERECREAEKAQQSYERLDNDTNATKADV EKAKQQLNLRTHMADENKNEYAAQLQNFNGEQ HKHFYVVIPQIYKQLQEMDERRTIKLSQYRGFA DSERKVIPIISKLEGMLAAKSVDERRDSQMVV DSFKSGFEPPGDFPFEDYSQHIYRTISDGTISASKQ ESGMDAKTTVGKAKGKLWLFQKKPKGPALED FSLPPEQRRKKLQQRIDELNRELQKESDQKDAL NKMKDVEYKPNQMGDPGSLQPKLAETMNNIDR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LRMEIHKNEAWLSEVEGKTGGRGDRRHSSDINH LVTQGRESPEGSYTDANQEVRGPPQQHGHNE FDDEFEDDDPLPAIGHCKAIYPFDGHNEGTAMK EGEVLIIIEEDKGDGWTRARRQNGEEGYVPTSYI DVTLEKNSKGS
3827	A	2	1584	INPVSSAVNGEAHSSHETRGQNSNALPSVLELL SQSCLIPAMSSYLNRNDSVLDMARHVPLYRALLEL LRAIASCAAMVPLLLPLSTENGEEEEEQSECQTS VGTLLAKMKTCVDITYNRLRSKRENVKTGVKP DASDQEPEGLTLLVPDIQKTAEIVYAATTSLRQA NQEKKLGEYSKKAAMKPKPLSVLKSLEEKYVAV MKKLQDFTFEMVSEDEDGKLGFKNYHYMSQV KNANDANSAARARRLAQEA VTLSTSLPLSSSSSV FVRCDEERLDIMKVLITGPADTPYANGCFEFDVY FPQDYPSSPPLVNLETTGGHSVRFPNPNLYNDGKV CLSILNTWHGRPEEKWNPQTSSFLQVLVSVQSLI LVAEPYFNEPGYERSRGTPSGTQSSREYDGNIRQ ATVKWAMLEQIRNPSPCFKEVIHKHFYLRVEIM AQCEEWIADIQYSSDKRVGRTMSHHAAALKRH TAQLREELLKLPCPEGLDPTDDAPEVCRATTGA EETLMHDQVKPSSSKELPSDFQL
3828	A	1415	845	PRVPATLVSLDPWHCFPTAGRLAGSTWVPPACT LQLGPSSEHELDNHRAPLLSLPSQESLSFTPWYLV ACKPLFHIFCPLFACFMQEGKVQYFLHLHSHMRL LNYYFFPFLAPESLMQALEDLDYLAALDNDGNL SEFGIIMSEFPLDPQLSKSILASCEFDVDEVLTIA AMVTGILNDYSFSFFANLH
3829	A	199	683	VDHTPVLSKPCQCFSSVKWGATLSARSQKTSIGIR LMVHVIEATELKACKPNGKSNPYCEISMGSQSYT TRTIQDTLNPKNWFNCQFFIKDLQDVLCLTLFD RDQFSPDDFLGRTEIPVAKIRTEQESKGPMTRRLL LHEVPTGEVWVRFDLQLEQKTL
3830	A	1747	404	RKMMEESGIETTPPGTTPPNPAGLAA TAMSSTPV PLAATSSFSPPNVSSMESFPPLAYSTPQPPLPPVRP SAPLPFVPPPAVPSVPPLVTSMPPVPSPSTAAAFG NPPVSHFPSTSA PNTLLPAPPSGPPISGFSVGSTY DITRGHAGRAPQTPLMPSFSAPSGTGLLPTPITQQ ASLTSLAQGTGTTSAITFPEEQEDPRITRGQDEAS AGGIWGFIKGVAGNPMVKSVDKTKHSVESMIT TLDPGMAPYIKSGGELDIVVTSNKEVKVA A VRD AFQEVFGLAVVVGEAGQSNIAQPVG Y AAGLK G AQERIDSLRRTGVIHEKQTA VSVENFIAELL PDK WFDIGCLVVEDPVHGIHLETFTQATPVPLEFVQQ AQLSTPQDYNLRW SGLLVTVGEVLEKSLNVS R TDWHMAFTGMSRRQMIYSAARA IAGMYKQRLP PRTV
3831	A	5	674	FWTRSAWHEGLQQMKANDPSLQEVNLYNIKNIP IPTLREFAKALETNTHVKKFLAATRSNDPVAIAF ADMLKVNTTLTSLNIESHFITGTGILALVEALKEN DTLTEIKIDNQRQQLGTAVEMEIAQMLEENSRI L KFGYQFTKQGPRTRVAAAITKNNDLAWQKDTQ EQTSIWQVVSQSLAGFN PQFEVQQGNARSWMEE LGKAFHQFVRRELKQTEGKLP
3832	A	164	782	EPWVPMDDVAESPERDPHSPEDDEEQPQGLSDDDI L RDSGSDQDL DGAGVRASDLEDEESAARGPSQEE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EDNHSDEEDRASEPKSQDQDSEVNLSRGPTSSP CEEEGDEGEEDRTSDLRDEASSVTRELDEHELDY DEEVPEEPAPAVQEDEAEKAGAEDDEEKGEGTP REEGKAGVQSVGEKESLEAAKEKKKEDDDGEID DEEMY
3833	A	122	1676	SQPPHFTQKMENKDTDSKKSEYEDDFEKDLE WLINENEKSDASIIEMACEKEENINQDLKENETV MEHTKRHSDPDKSLQDEVSPRRNDIISVPGIPLD PISDSSENSFQESKLESQKDLEEEEDDEEVRRYIM EKIVQANKLLQNQEPVNDKREKRLKFKDQLVDL EVPPLDTTTSKNFYFENERNMFGKLSQLCISNDF GQEDVLLSLTNGSCEENKDRITL VERDGKFELN LQDIASQGFLLPINNANSTENDPQQLPRSSNSSV SGTKKEDSTAKIHAVTHSSTGEPLAYIAQPLNR KTCPSA VNSDRSKGNGKSNHRTQSAHISPTST YCLSPRQKELQKQLEEKREKLKREEERRKIEEEK EKKRENDIVFKA WLQKKREQVLEMRRIRAKEI EDMNSRQENRDPQAFRL WLKKKHHEEQMKERQ TEELRKQEECLFFLKGTTEGRERAFKQWLRRKRM EKMAEQQA VRERTRQLRLEAKRSKQLQHLYM SEAKPFRFTDHYN
3834	A	575	774	RSRTEELSNGILKAMSKDLVTFGDVA VNFSSQEE WEWLNPAQRNLYRKVMLENYRSLVSLGKDMSP
3835	A	2	100	ASDFYLRYYVGHKGKFGHEFLEFEFRPDGVYV
3836	A	91	749	RPTPGHGD FWMQPLTKDAGMSLSSVTLASALQV RGEALSEEEIWSLLFLAAEQLEDLRNDSSDYVV CPWSALLSAAGSLSFQGRVSHIEAAPFKAPELLQ GQSEDEQPDASQMHVYSLGMTLYWSAGFHVPP HQPLQLCEPLHSILLTMCEDQPHRRCTLQSVLEA CRVHEKEVSVYPAPAGLHRRLLVGLVLGTISEVS REPCFSSSSCWSCVAIKI
3837	A	3	1214	SLGCTNSARGKGQDDEVRTL MANGAPFTTDWFS KLRVSCGYIGDNCKNGADVNAKMDLKM TALH WATERHHRDVVELLIKYGADVHAFSKFDKSAFD IALEKNNAEILVILQEAMQNQVNVNPERANPVT PVSMAAPFIFTSGEVVNLASLISSTNTKTTSGDPH ASTVQFSNSTTSVLATLAALAEASVPLSNHRAT ANTEEIEGNSVDSSIQQVMGSGGQRVITIVTDGV PLGNIQTSIPTGGIGHPPFIVTVQDGQQVLTVPAGK VAEETVIKEEEEEELPLTKKPRIGEKTNSVEESKE GNERELLQQQLQEANRRAQEYRHQLLKKEQEAE QYRLKLEAIARQQPNGVDFTMVEEVAEVDVAVV VTEGELEERETKVTGSAGATGPPTRVSMATVSS
3838	A	1	1332	MIEDNKENKDHSLERGRASLIFSLKNEVGGLIKA LKIFQEKHVNLLHIESRKSRRRNSEFEIFVDCDIN REQLNDIFHLLKSHTNVLSVNLDPNFTLKEDGME TVPWFPPKKISDLHDHCANRVLMYGSELDADHPGF KDNVYRKRRKYFADLAMNYKHGDPPIPKVEFTEE EIKTWGTVFQELNKLYPHACREYLKNLPLLSKY CGYREDNIPQLEDVSNFLKERTGFSIRPVAGYLS RDFLSGLAFRVFHCTQYVRHSSDPFYTPEDTCH ELLGHVPLLAEPFSAQFSQEIGLASLGASEEAVQ KLATCYFFTVEFGLCKQDQGLRVFGAGLLSSISE LKHALSGHAKVKPFDPKITCKQECLITTFQDVYF VSESFEDAKEKMREFTKTIKRPFGVKYNPYTRSI

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				QILKDTKSITSAMNELQHDLDVSDALAKVSRKPSI
3839	A	3093	520	MVNFTVDQIRAIMDKKANIRNMSVIAHVDHGKSLTDSLVCAGILASARAGETRFTDTRKDEQERCITIKSTAILFYELSENDLNFQKSKDGAGFLNLIDSPGHVDFSSEVTAALRVTDGALVVVDCVSGVCVQTETVLRQAIAERIKPVLMMNKMDRALLELQLEPEELYQTFQRIVENVNVIISTYGEGESGPMGNIMIDPVLGTVGFGSGLHGWAFTLKQFAEMYVAKFAAKGEGQLGPAERAKKVEDMMKKLWGDRYFDPANGKFSKSATSPGKKLPRTFCQLIDPIFKVFDAIMNFKKEETAKLIEKLDIKLDESKDKGKPLLKAVMRRWLPAGDALLQMITIHLPSPVTAQKYRCELLEYEGPPDDEAAMGIKSCDPKGPLMMYISKMVP TSDKGRFYAFGRVFSGLVSTGLKVRIMGPNYTPGKKEDLYLKPIQRTILMMGRYVEPIEDVPCGNIVGLVGVDQFLVKTGTTTTFEHAHNMRVMKFSVSPVVRVAVEAKNPADLPKLVEGLKRLAKSDPMVQCIIEESGEHIIAGAGELHLEICLKDLEEDHACIPIKSPVVSRYRETVSEESNVLCLSKSPNKHNLRYMKARPPDGLAEDIDKGEVSARQELKQRARYLAEKYEWDVAEARKIWCFGPDGTGNILTDITKGVQYLNEIKDSVVAGFQWATKEGALCEENMRGVRFDVHDVTLHADAIHRGGGQIPTARRCLYASVLTAQPRLMETIYLVEIQCEQVVGGIYGVNLNRKRGHVFEESQVAGTPMFVVKAYLPVNESFGFTADLRNSTGQQAFFQCVFDHWQLPGDPFDNSSRPSQVVAETRKRKGLKEGIPALDNFLDKL
3840	A	2	753	SSTRSDFCCSEAIQGSLTRRERRASGVRTRRSQSSAMASKILLNVQEEVTCPICLELLTEPLSLDCGHS LCRACITVSNKEAVTSMGGKSSCPVCGISYSFEHLQANQHLANIVERLKEVKLSPDNGKKRDLCDH HGEKLLLFCKEDRKVICWLCERSQEHRGHHTVLT EEEVFKECQEKLAQVLKRLKKEEEEAKELEADIR EEKTSWKYQVQTERQRIQTEFDQLRSILNNEEQRELQRL EEEKKT
3841	A	2	405	GKAFSCFTYLSQHRRTHMAEKPYECKTCKKAFFS HFGNLKVHERIHTGEKPYECKEKRKAFFSWLTCL LRHERIHTGKKSYECQQCGKAFTSRFLRGHEKTH TGEKMHECKECKGKALSSSLHHRKHRTHWRTDL
3842	A	311	88	AVLKNMAPMTALGLLDLHILNLILFLSAGEDFTSVSEIMMYILLVFLTLWLLIEMIYCYRKVSKAEAAQENA
3843	A	3	1175	APIRNSRIDDFVRRVESKATSARCGLWGSGRRRPASGMFRGLSSWLGLQQPVAGGGQPNGDAPPEQPSETVAESAEEELQQAQDQELLHQAKDFGNLYLFNFASAAATKKITESVAETAQTIKKSVEEGKIDGIIDKTIIGDFQKEQKKFVEEQHTKKSEAAVPPWVDTNDEETIQQQLALSADKRNFLRDPAGVQFNFDFDQMPVALVMLQEDELSSKMRFALVPKLVKEEVFWRNYFYRVSLIKQSAQLTALAAQQQAAGKEEK SNGREQDLPLAEAVRPKTPPVVKSQKLTQEDEEEISTSPGVSEFVSDAFDACNLNQEDLRKEMEQLVLDKKQEETAVLEEDSADWEKELQQELQEYEV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				VTSEKRDENWDKEIEKMLQEEN
3844	A	798	148	LPQAQIPEAWLLANVVVLILVPLKDRLIDPLLRCKLLPSALQKMALGMFFGFTSVIVAGVLEMERLHYIHNETVSQQIGEVLYNAAPLSIWWQIPQYLLIGISEIFASIPGLEFAYSEAPRSMQGAIMGIFFCLSGVGSLLGSSLVALLSLPGGWLHCPKDFGNINNCRMDLYFFLLAGIQAVTALLFVWIAGRYERASQGPASHSRFSRDRG
3845	A	3	1934	PEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFFKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYSLQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRCLKHRGSSLHPRFKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNPRTRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG
3846	A	3	1934	PEDSAPQYSRLFPNASQHITPSYNYAPNPDKHWIMRYTGPMKPIHMEFTNMLQKRRLQTLMSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMPYEFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAPTILDIAGLDIPADMDGKSILKLLDTERPVNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQRVKDLQRAEYQTACEQLGQKWQCVEDATGKLKLHKCKGPMRLGGSRALSNLVPKYYGQGSEACTCDSGDYKLSLAGRRKKLFFKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAAQPRNLTKRHWPGAPEDQDDKDGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLKYSLQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKKRPEECDCHKISYHTQHKGRCLKHRGSSLHPRFKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLGPFCACTSANNTYWCMRTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGYKQCNPRTRNMDLGLKDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG
3847	A	1	1257	MVFSAVLTAFTGTSTNTTFVYENTYMNITLPPPFQHPDLSPLLRYSFETMAPTGLSSLTVNSTAVPTTAAAFKSLNLPQITLSAIMIFILFVSFLGNLVVCLMVYQKAAMRSAINILLASLAFADMLLAVLNMPFALLVTILTTRWIFGKFFCRVSAMFFWLFVIEGVAILLIISIDRFLIIVQRQDKLNPYRAKVLIASVWATSEFCVAFPLAVGNPDLQIPSRAPQCVFGYTTNPGYQAYV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				ILISLISFFIPFLVILYSFMGILNLTLRHNALRIHSYPE GICLSQASKLGLMGLQRPQMSIDMGFKTRAFTT ILILFAVFIVCWAPFTTYSLVA TFSKHFFYYQHNF EISTWLLWLCYLKSALNPLIYYWRIKKFHDACLD MMPKSFKFLPQLPGHTKRRIRPSAVVYVCGEHR VV
3848	A	3	2827	SSAVAARRRRSWASLVLAFLGVCLGITLAVDRS NFKTCEESSFCKRQRSIRPGLSPYRALDLSLQGP DSLTVHLIHEVTKVLLVLELQGLQKNMTRFRIDE LEPRRPRYRVPDVLVADPPIARLSVSGRDENSVE LTMAEGPYKIILTARPFRLDLEDRLSLLSVNARG LLEFEHQRAPRVSQGSKDPAEGDGAQPEETPRD GDKPEETQGKAEEKDEPGAWEETFKTHSDSKPYG PMSVGLDFSLPGMEHVYGIPEHADNRLKVTG GEPYRLYNLDVFQYELYNPMALYGSVPVLLAHN PHRDLGIFWLNAAEWVDISSNTAGKTLFGKMM DYLQGSGETPQTDVRWMSETGIIDVFLLLGPSISD VFRQYASLTGTQALPPLFSLGYHQSRWNYRDEA DVLEVDQGFDDHNLPCDVIWLDIEHADGKRYFT WDPSPFPQPRITMLERLASKRRKLVAIVDPHIKVD SGYRVHEELRNGLYVKTRDGSDEYEGWCWPGS AGYPDFTNPTMRAWWANMFSYDNYEGSAPNLF VWNDMNEPSVFNGPEVTMLKDAQHYGGWEHR DVHNIYGLYVHMATADGLRQSRGGMERPFVLA RAFFAGSQRFAGAVWTGDNTAEWDHLKISIPMCL SLGLVGLSFCGADVGGFFKNPEPELLVRWYQMG AYQPPFFRAHAHLDTGRREPWLLPSQHNDIIRDAL GQRYSLLPFWYTLTYQAHREGIPVMRPLWVQYP QDVTTFNIDDQYLLGDALLVHPVSDSGAHGVQV YLPQGGEVWYDIQSYQKHGHPQTLYLPVTLSSIP VFQRGGTIVPRWMRVRRSSECMKDDPITLFVALS PQGT AQGELFLDDGHTFNYQTRQEFLLRRFSFG NTLVSSADPEGHFETPIWIERVVIIGAGKPAAVV LQTKGSPESRLSFQHPETSVLVLRKPGINVASD WSIHLR
3849	A	1	1717	RARNARGCWGVCRSGFSSAVCGAARMEQVAEG ARVTAVPVSAADSTEELAEVEEGVGVVGEDNDA AARGAEAFGDSEEDGEDVFEVEKILDMKTEGGK VLYKVRWKGYTSDDDTWEPEIHLEDCKEVLLEF RKKIAENKAKAVRKDIQRLSLNNDIFEANSDDQ QSETKEDTSPKKKKKKLRQREEKSPDDLKKKKA KAGKLKDKSKPDLESSLESVFDLRTKKRISEAK EELKESKKPKKDEVKETKELKKVKKGEIRDLKT KTREDPKENRKTKEKFVESQVESESVLNDSPF PEDDSEGLHSDSREEKQNTKSARERAGQDMGLE HGFELPLDSAMSAEEDTDVRGRRKKKTPRKAED TRENKLENKNAFLEKKTVPKKQRNQDRSKSAA ELEKLMPVSAQTPKGRRLSGEERGLWSTDSAE DKETKRNESKKPKKDEVKETKELKKVKKGEIRD LKTKTREDPKENRKTKEKFVESQVESESVLND SPFPEDDSEGLHSDSREEKQNTKSARERAGQDM GLEHGFELPLDSAMSAEEDTDVRGRRKKKTPRK AEDTRENKLENKNAFLEKKTVPKKQRNQDRSK SAAELEKLMPVSAQTPKGRRLSGEERGLWSTDS AEEDKETKRNESKKPKKDEVKETKELKKVKKGE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				IRDLKTKTREDPKENRRTKKEKFVESQVESESSV LNDSPFPED/RQ*RAFTRQOREKSPDDLKKKKA KAGLKD KSKPDLESSLES L VF DLRTKKRISEAK EELKESKKPK
3850	A	1113	3975	PAAAAAAGAAAAAAGRPSFTPCFSPSLAVEPS RRTRLGSDPAQAMAGNVKKSSGAGGGSGSGGS GSGGLIGLMKDAFQPHHHHHHLSHPHPPGTVDK KMVEK CWKLMDKVVR L C Q N P K L A L K N S P P Y I L DLLPD TY Q H L R T I L S R Y E G K M E T L G E N E Y F R V F MENLMKKTKQTISLFKEGKERMYEENSQPRRNL TKLSLIFSHMLAELKGIFPSGLFQGDTRITKADA AEFWRKAFGEKTIVPWKSFRQALHEVHPISGLE AMALKSTIDLTCNDYISVFEFDIFTRLFQPWSSLL RNWNSLAVTHPGYMAFLTYDEVKARLQKFIHKP GSYIFRLSCTRLGQWAIGYVTADGNILQTIHPNKP LFQALIDGFREGFYLPDGRNQNPDLTGLCEPT QDHIKVTQEYEL YCEMGSTFQLCKICAENDKD VKIEPCGHL MCT SCLTSWQESGQGCPFCRCEIK GTEPIVDPFDPGRSGSLLRQGAEGAPSPNYDDD DDERADDTLFMMKELAGAKVERPPSPFMAPQA SLPPVPRLDLLPQRVCVPSSASALGTASKAASGS LHKDKPLPVPTLRDLPPPPPPDRPYSVGAESRPQ RRPLPCTPGDCPSRDKLPPVPSSRLGDSWLPRPIP KVPVSAPSSDPWTGRELTNRHSLPFSLPQMEP RPDVRLGSTFSLDTSMSMNSSPLVGPECDHPKI KPSSSANAIYSLAARPLPVPKLPPEGEQCEGEEDTE YMT PSSRPLRPLDTSQSSRACDCDQIDSCTYEA MYNIQSQAPSITESSTFGEGNLA A A H A N T G P E E S ENEDDG Y D V P K P P V P A V L A R R T L S D I S N A S S / F G LFVLERDP*PQNVTEGSQVPERPPKPFPRINSE KAGSCQQSGPAASAATA/SPQLSSEIENLMSQG YSYQDIQKALVIAQNNIEMAKNILREFVSISSPAH VAT
3851	A	2	2781	GRVGSMDGAMGPRGLLLCMYLVSLILQAMPA LGSATGRSKSSEKRQAVDTAVDGVFIRSLKVNC KVTSRFAHYVVT SQV V N T A N E A R E V A F D L E I P K TAFISDFAVTADGNAFIGDIKDKVTAWKQYRKA AISGENAGLVRASGR T M E Q F T I H L T V N P Q S K V T F QLTYEEVLKRNHMQYEIVKVKPKQLVHHFEIDV DIFEPQGISKLDAQASFLPKELAAQTIKKSFSGKK GHVLFRTVSQQQSCPTCSTSLNGHFKVTYDVS RDKICDLLVANNHFAHFFAPQNL TNMKNVVFV IDISGSMRGQKV K Q T K E A L L K I L G D M Q P G D Y F D LVLFGTRVQSWKGS LVQASEANLQAAQDFVRGF SLDEATNLNGGLLRGIEILNQVQESLPESLNHASI LIMLTDGDPTEGVTD RSQILKNVRNAIRGRFPLY NLGFGHNVDNFLEVM SMENNGRAQRIYEDHD ATQQLQGFYSQVAKPLLVDVDLQYPQDAVLALT QNHKKQYYEGSEIVVAGRIADNKQSSFKADVQA HGEGQEFSITCLVDEEEMKKLLRERGHMLNENH ERLWAYLTIQELLAKRMKV DREVRANLSSQALR MSLDYGFV T P L T S M S I R G M A D Q D G L K P T I D K P S E DSPPLEMLGPRRTFVLSALQSP THSSSNTQRLPD RVTGVD T D P H I I H V P Q K E D T L C F N I N E E P G V I L S LVQDPNTGFSVNGQLIGNKARSPGQHDGTYFGR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LGIANPATDFQLEVTQNTITLNPFGGGPVFWSWRD QAVLRQDGVVVTINKKRNLVVSVDGDTFEEVVA LHRVWKGSSVHQDFLGLLMCWDSIGMSSPGR KGCWGWQFFHPIRFLKVS*HPPPGSDPQKAQMPT MVVRNPPGLTVTRGLQKDYSKDPWHGAEVSC WFIHNNGA*ITDCAVTDYIVPDIF
3852	A	39	1735	TQVAEAGRGEGV VAGAETGR PQSAGM NLELLES FGQNYPEEADGTLDCISMALCTCFNRWGTL LAV GCNDGRIVWDFLTRGIA*NKFSAHHPVCSLC WSRDGHKLVSASTDNIVSQWDVLSGDCDQRF RF PSPILKVQYHPRDQNKVLVCPMK SAPVMLT LSD SKHVLPVDDSDLN VVASFDRRGEYIYTGNAK GKILVLKTDSDQLVASFRVTTGTSNTTAKSIEFA RKGSCFLINTADRIIRVYDGREILT CGRDGEPEPM QKLQDLVNRTPWKKCCFSGDGEYIVAGSARQH ALYIWEKSIGNLVKILHGTRGELL LDVAWHPVRP IIASISSGVVSIWAQNQVENWSAFAPDFKELDEN VEYEERESEFDIEDEDKSEPEQTGADAAEDEEVD VTSVDPIAFCSSDEELED SKALLYLPIAPEVEDP EENPYGPPDAVQTS LMDEGASSEKKRQSSADG SQPPKKKPKTTNIELQGV PNDEVHPLLGVKG DG KSKKKQAGRPK GSKGKEKDS PFKPKLYKGDRGL PLEGSAKGKVQAE LSQPLTAGGAISELL
3853	A	45	2603	PLLFTCGREVRARDPEKEGTIVVAGLK VQVQPRF LWILCFSMEETQ GELTSSCGSKT MANVSLAFRDV SIDLSQEEWECLDAVQRDL YKDVMLENYSNLVS LDLEYKYITKNLLSEKNVCKIYLSQLQTGEKSKN TIHEDTIFRNLQCKHEFERQERHQMGCVSQMLI QKQISHPLHPKIHAREKSYECKE CKRAFRQQSYLI QHLRIHTGERPYK CMECGKAFCRVGDLRVHHTI HAGERPYECKE CGKAFLRHYHLTEHQRIHSGVK PYECKE CGKAFSRVRDLRVHQTIHAGERPYECK ECGKAFLRHYQLTEHQRIHTGERPYECKVCGKT FRVQRHISQHQIHTGVKPYKCNECGKAFSHGS YLVQHQQIHTGEKPYECKE CGKSFSFHAELARH RRIHTGEKPYECRECGKAFLRQTELTRHHRHTHTG EKPYECKE CGKAFICGYQLTLHLRHTHTGEIPYEC KECGKTFSSRYHLTQHYRIHTGEKPYICNECGKA FRLQGELTRHHRHTCEKPYECKE CGKAFIHSNQ FISHQRIHTSESTYICK ECGKIFSRRYNTLQHF KIH TGEKPYICNECGKA FRFQTELQHHRIHTGEKPY KCTECGKA FIRSTHLTQHHRHTGEKPYECTECG KTFSTRHYHLTQHHRGHTGEKPYICNECGNAFICS YRLTLHQRIHTGELPYECKE CGKTFSSRYHLTQH FRLHTGEKPYSCKECGNAFRLQAE LTRHHIVHTG EKPYKCKE CGKAFSVNSELTRHHRHTGEKPYQC KECGKA FIRSDQLTLHQKILVRNPMHNVKRIR WPLENAL*QRICNL RNFVTEHVGIPFTSCSQFI RNYFVC
3854	A	108	894	LQSCWVP GIPWPSV GWSLWLDLPSC EIHSA SL S AVLQGPQCSEML WPKNLTSWDDSSSVSSGISDTI DNLSTDDINTSSSISSYANTPASSRKNLDVQ TDAE KHSQVERNLSWSGDDVKKSDGGSDSGIKMEPGS KWRRNPSDVSDSDKSTSGKKNPVISQTGSWRR GMTAQVGITMPRTKASAPAGALKTPGTGKR PGL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SIGPGAPTPAAPQLARMAWAFSLSAASTPAVSP STSPSAVEGSPA TILPLASSPPPRTP*LPLSELTV* RPQELVRGRGCLGPGAPTPAAPQLARMAWAFS LSAASTPAVSPSTSPSAVEGSPA TILPLASSPPPRTP
3855	A	1	772	FRGGDGAPGVLPKPGNLPFPLPPLQYPPSTLSHS DNLAMTSRSTARPNQGPQASKICQFKLVLLGESA VGKSSLVLRVKGQFHEYQESTIGAFLTQSVCL DDTTVKFEIWDTAGQERYHSLAPMYRGAQAAI VVYDITNQETFARAKTWVKELQRQASP/SIVVGL AGNKADLANKRMVEYEEAQAYADDNSLLFMET SAKTAMNVNDLFLAIA*EVAKRNVNPQNLG/GVA AGRSRGVDLHEQS/QQNKSSQCCSN
3856	A	2815	352	LGLEAAARPRPGGPAAMQDGNFLLSALQPEAGV CSLALPSDLQLDRRGAEGPEAERLRAARVQEQQ RARLLQLGQQPRHNGAAEPEPEAETARGTSRGQ YHTLQAGFSSRSQGLSGDKTSGFRPIAKPAYSPA SWSSRSAVDLSCSRRLSSAHNGGSFAGAAGYGG AQPTPPMPTRPVSFHERGGVGSRADYDTLSLRS RLGPGGLDDRYSLVSEQLEPAATSTYRAFAYER QASSSSRAGGLDWPEATEVSPSRITRAPAVRTL QRFQSSHRSGVGGAVPGAVLEPVARAPSVRSL LSLADSGHLPDVHGFNSYGSHTLQRLSSGFDDI DLPSAVKYLMA SDPNLQVLGAAYIQHKCYSDAA AKKQARSLQAVPRLVKLFNHANQEVQRHATGA MRNLIYDNADNKLALVEENGIFELLRTLREQDDE LRKNVTGILWNLSSSDHLKDRLAKKTPLE/QLTD LGV*APLSGAGGPPLIQQNASEAEIFYNATGFPR NLSSASQATRQKMRCHGLVDALVTSINHALDA GKCEDKSVENAVCVLRNLSYRLYDEMPPSALQR LEGRGRDLA GAPPGEVVGCFTPQSRRLRELPLA ADALTFAEVSKDPKGLEWLWSPQIVGLYNRLQ RCELNRHTTEAAAGALQNTTGG/DPRGPGGLSRL ALEQERILNPLLDRTADHHQLRSLTGLIRNLS RNARNKDEMSTKVASHLNEKLPGSVGEKSPAE VLVNIAVFNNLGWLASPI/ALARDLLYFDGLRK LFIKKKRDPDSEKSSRAASSLLANLWQYNKLH RDFRAKGYRKEDFLGP
3857	A	1034	204	VAVTLLSQLPSAIQRTAAWEMRAPLTFRVPLALD LIKPEHCTVNVDNSLSIPVIAELVVRKPSEKGM QQKKKTKDLGFRAGKESKTEWRK*GLQDMSAQ MFALPLK*PVTA AFHDSSMPSSLLQIEMEQLFLE ARLQ/PDSKSEARRNQCD SMLLRNQQLCSTCQE MKMVQPRTMKIPDDPKASFENCMSYRMSLHQP KFQTTPEPFHDDIPTENIHLQNL/PILGPRTAVFHG LLTEAYKTLKERQRSSLPRKEPIKTTEAVSGRSS SPRLPERK
3858	A	203	3469	SHQEIQNSAMAPRKRGGRGISFIFCCFRNNDHPE ITYRLRNSNFALQTMEPALPMPPVEELDMVFSE LVDELDTDKHREAMFALPAEKKWQIYCSKKK DQEENKGATSWPEFYIDQLNSMAARKSLLALEK EEEEERSKTIESLKTALRTKPMRFVTRFIDLGLS CILNFLKTMDYETSESRIHTSLIGCIKALMNNSQG RAHVLAHSESINVIAQSLSTENIKTKVAVLEILGA VCLVPGGHKKVLQAMLHYQKYASERTRFQTLIN

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DLDKSTGRYRDEVSLKTAIMSFINAVLSQGAGVE SLDLRLHLRYEFLMLGIHPVMDKLRKHENSTLD RHLDFEFMLRNEDELEFAKRFELVHIDTKSATQM FELTRKRLTHSEAYPHFMSILHHCLOMPYKRSGN TVQYWLLLDRIHQIIVIQNDKGQDPDSTPLENFNI KNVVRMLVNENEVKQWKEQAEMRKEHNELQ QKLEKKERECDAKTQEKEEMMQTLNKMKEKLE KETTEHKQVKQVADLTAQLHELSRRAVCASIP GGSPGAPGGPFSSVPGSLLPPPPPPPLPGGMLPP PPPPLPPGPPPPPGPPPLGAIMPPPGAPMGLALK KKSIPQPTNALKSFNWSKLPENKLEGTWTEIDD TKVFKILDLEDLERTFSA YQRQDFFVNSNSKQK EADAIDDTLSSKLKVKELSVIDGRRQAQNCNILLS RLKLSNDEIKRAILTMDEQEDLPKDMLEQLLKFFV PEKSDIDLLEEHKHELDMAKADRFLFEMSRINH YQQLQSLYFKKKFAERVAEVKPKVEAIRSGSEE VFRSGALKQLLEVVLAFGNMNGQQRGNAYGF KISSLNKIADTKSSIDKNITLLHYLITIVENKYPSV LNLNEELRDIPQA AKVNMTELDKEISTLRSGLKA VETELEYQKSQPPQPGDKFVS VVSQFITVASFSFS DVEDLLAEAKDLFTKAVKHFGEEAGKIQPDFF GIFDQFLQAVSEAKQENENMRKKKEEEERRARM EAQLKEQRERERKMRKAKENSEESGEFDDL VSA LRSGEVFDKDL SKLKRNRKRITNQMTDSSRERPI TKLNF
3859	A	1279	141	RVEHLSEFLVDIKPSLTFDVIPLDPYGPAGSDPS LEFLVVSEETYRGGMAINRFRLENDLEALALYQI QLLKDLRHTENEDKVSSSSFRQRLGNLLRPPY ERPCLPTCLYVIGLTGISGSGKSSIAQRLKGLGAF VIDSDHLGHRA YAPGGPAYQPVVEAFGTDLHK DGIINRKVLGSRVFGNKKQLKILTDIMWPILAKLA REEMDRAVAEGKRVVIDAAVLLEAGWQNLVH EVWTAVIPETEAVRRIVERDGLSEAAAQSRLQSQ MSGQQLVEQSHVVLSTCGSRISPNAWRKPGPS CRSAFPRLIRPSTEFKSVGPDWLELTSDPVVRRN GGLDAHPSGPEVQAILCRTWPGLVDTGSLPNTL VFGQH
3860	A	1	3881	MGQKSVGASYVQIPLVPPLSRHPKGLGHEDRWS SYCLSSLA AQNICTSKLHCPAAPEHTDPSEPRGSV SCCSLLRGLSSGWSSPLLPAVCNPNKAIPTVDA KTTEILVANDKACGLLGYSQDLIGQKLTQFFLR SDSDVVEALSEEHMEADGHAAVFGTVVDIISRS GEKIPVSVWMKRMQRERRCCVVVLEPVERVST WVAFAQSDGTVTSCDSLFAHLHGYVSGEDVAGQ HITDLIPSVQLPPSGQHIPKNLKIQRSVGRARDGT TFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWV FCTISGLITLLPDGTIHGINHSFALTFLGYGKTELL GKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDV GNESGCCERTLDPWQQQDPAEGGQDPRINVVLA GGHVVPRDEIRKLMESQDIFTGTQTELIAGGQLL SCLSPQAPGVNDVPEGSLPVHGEQALPKDQGIT ALGREEPVAIESPGQDLLGESRSEPVDVKPFASCE DSEAPVPAEDGGSDAGMCGLCQKAQLERMGV GPSGSDLWAGAAVAKPQAKGQLAGGSLLMHCP CYGSEWGLWWRSQLAPSPSGMAGLSFGTPTLD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EPWLGVENBREELQTCCLIKEQLSQLSLAGALDVP HAELVPTECQAVTAPVSSCDLGGRLCGGCTGS SSACYALATDLPGGLEAVEAQEVDVNSFSWNLK ELFFSDQTDQTSSNCSCATSELRETPSSLA VGSDP DVGSLQEQGSCVLDDRELLLLTGTCVDLGQGR FRESCVGHDPTEPLEVCLVSSEHYAASDRESPGH VPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMR GAAGLQREIQEGAYSGSCYHRDGLRLSIQFEVRR VELQGPTPLFCCWL VKDLLHSQRDSAARTLFL ASLPGSTHSTAAELTGPSLVEVLRARPWFEEPPK AVELEGLAACEGEYSQKYSTMSPLGSGAFGFVW TAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLG KVTLEIAILSRVEHANIUKVLDIFENQGGFFQLVME KHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\Q SRLVSAVGYLRKLDIIHRDIKDENVIAEDFTIKLI DFGSAAYLERGKLFYTCGTIEYCAPEVLMGNPY RGPELEMWSLGVTLTYLVFEENPFCELEETVEAA IHPPYLVSKEMLSVSGLLQVPERRTTLEKLV DPWVTQPVNLADYTWEVFRVKNKPESGVLSAAS LEMGNRSLSDVAQAQELCGGPVPGAPNGQGCL HPGDPRLTS
3861	A	1	3881	MGQKSVGASYVQIPLVPPLSRHPKGLGHEDRWS SYCLSSLA AQNICTSKLHCPAAPEHTDPSEPRGSV SCCSLLRGLSSGWSSPLLPAVCNPNKAIFTVDA KTTEILVANDKACGLLGYSQDLIGQKLTQFFLR SDSDVVEALSEEHMEADGHA AVVFGTVVDIISRS GEKIPVSVWMKRMQRERRLCCVVVLEPVERVST WVAFQSDGTVTSCDSLFAHLHG YVSGEDVAGQ HITDLIPSVQLPPSGQHIPKNLKIQRSVGRARDGT TFPLSLKLKSPSSEEATTGEAAPVSGYRASVWV FCTISGLITLLPDGTHGINHSFALTFGY GKTELL GKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDV GNESGCGERTLDPWQGDPAEGGQDPRINNVLA GGHVVPREIRKLMESQDIFTGTQTELIAGGQLL SCLSPQAPGVNDNPEGSLPVHGEQALPKDQKIT ALGREEPVAIESPGQDLLGESRSEPVDVKPFASCE DSEAPVPAEDGGSDAGMCGLCQKAQLERMGSV GPSGSDLWAGAAVAKPQAKGQLAGGSLLMHCP CYGSEWGLWWRSQLAPSPSGMAGLSFGTPTLD EPWLGVENBREELQTCCLIKEQLSQLSLAGALDVP HAELVPTECQAVTAPVSSCDLGGRLCGGCTGS SSACYALATDLPGGLEAVEAQEVDVNSFSWNLK ELFFSDQTDQTSSNCSCATSELRETPSSLA VGSDP DVGSLQEQGSCVLDDRELLLLTGTCVDLGQGR FRESCVGHDPTEPLEVCLVSSEHYAASDRESPGH VPSTLDAGPEDTCPSAEEPRLNVQVTSTPVIVMR GAAGLQREIQEGAYSGSCYHRDGLRLSIQFEVRR VELQGPTPLFCCWL VKDLLHSQRDSAARTLFL ASLPGSTHSTAAELTGPSLVEVLRARPWFEEPPK AVELEGLAACEGEYSQKYSTMSPLGSGAFGFVW TAVDKEKNKEVVVKFIKKEKVLEDCWIEDPKLG KVTLEIAILSRVEHANIUKVLDIFENQGGFFQLVME KHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAG\Q SRLVSAVGYLRKLDIIHRDIKDENVIAEDFTIKLI DFGSAAYLERGKLFYTCGTIEYCAPEVLMGNPY

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RGPELEMWSLGVTLTYTLVFEENPFCELEETVEAA IHPPYLVSKEMLMSLVSGLLQVPERRTTLEKLV DPWVTQPVNLADYTWEVFRVKNPESGVLSAAS LEMGNRSLSDVAQAQELCGGPVPGAPNGQGCL HPGDPRLTTS
3862	A	399	2069	TMDRSKRNSIAGFPFRVEARLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFFRLTRLDDFTCEKIGSG FFSEVFKVRHRASQVMALKMNTLSSNRANML KEVQLMNRLSHPNILRYINSGNLEQLLDSNLHLP WTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNC LIKRDENGYSAAVADFGLAEKIPDVSMGSEKLA VVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEII ARIQADPDYLPRTENFGLDYDAFQHMVGDCPPD FLQLTFNCCNMDPKLRPSFVEIGKTLLEILSRLQE EEQERDRKLQPTARGLLEKAPGVKRLSSLDKIP HKSPCPRRTIWLRSQSDIFSRKPPRTVSVLDPYY RPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSK SVISLVFDLDAPGPGTMPLADWQEPLAPPIRRWR SLPGSPEFLHQEACPFVGREESLSDGPPRLSSLK YRVKEIPPFRASALPAAQAHEAMDCSILQEENG GSRPQGTSPCPAGASEEMEVEERPAGSTPATFSTS GIGLQTQKQDG
3863	A	399	2069	TMDRSKRNSIAGFPFRVEARLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFFRLTRLDDFTCEKIGSG FFSEVFKVRHRASQVMALKMNTLSSNRANML KEVQLMNRLSHPNILRYINSGNLEQLLDSNLHLP WTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNC LIKRDENGYSAAVADFGLAEKIPDVSMGSEKLA VVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEII ARIQADPDYLPRTENFGLDYDAFQHMVGDCPPD FLQLTFNCCNMDPKLRPSFVEIGKTLLEILSRLQE EEQERDRKLQPTARGLLEKAPGVKRLSSLDKIP HKSPCPRRTIWLRSQSDIFSRKPPRTVSVLDPYY RPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSK SVISLVFDLDAPGPGTMPLADWQEPLAPPIRRWR SLPGSPEFLHQEACPFVGREESLSDGPPRLSSLK YRVKEIPPFRASALPAAQAHEAMDCSILQEENG GSRPQGTSPCPAGASEEMEVEERPAGSTPATFSTS GIGLQTQKQDG
3864	A	3	911	SWNMDSDSCAAFAHPEEYSPSCKRRRTVEDFNK FCTFVLAAYGYIPYKPEELPLRSSPANSTAGTI DSDGWDAGFSDIASSVPLPVSDRCFSLQPTLLQ RAKPSNFLDRKKTDKLKKKKKKRKRSDAPGK EGYRGGLLKLEAADPYVETPTSPTLQDIPQAPSD PCSGWSDTPSSGSCATVSPDQVKEIKTEGKRTI VR/QEAQLMARNDGNFSSLESIFPS\DDDSWDLV TCFCMKPFAGRPMIECNECHTWIHLSCAKIRKSN VPEVFVCQKCRDSKFDIRRSNRSRTGSRKFLD
3865	A	3	3573	QERLRSRSPDRAAREAGSARGRQPKRTERVEQ FLTIARRRGRRSMPVSLEDSGEPTSCPATDAETAS EGSVESASETRSGPQSASTAVKERPASSEKVKGG DDHDDTSDSDGLTLKELQNRLRRKREQEPT RPLKGIQSRLRKKRREGPAETVGSEASDTVEGV LPSKQEPENDQGVVSQAGKDDRESKLEGKAAQD IKDEEPGDLGRPKPECEGYDPNALYCICRQPHNN

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RFMICCDRCEEWFHGDCVGISEARGRLLERNGE DYICPNCTILQVQDETHSETADQQEAKWRPGDA DGTDCSTIGTIEQKSSDQGIKGRIEKAANPSGKK KLKIFQPGPGPVPTQLPVLWQVLEIAVSRISAFT LLHCISCKVIEAPGASKCIGPGCCHVAQPDVSYCS NDCILKHAAATMKFLSSGKEQKPKPEKMKMK PEKPSLPKCGAQAGIKISSVHKRPAPEKKETTVK KAVVVPARSEALGKEAACESSTPSWASDHNYNA VKPEKTAAPSPSLLYKSTKEDRRSEEKAAATAAS KKTAPPGSTVGKQPAPRNLPKKSSFANVAAAT PAIKKPPSGFGKTIPKRPWLSATPSSGASAAARQAG PAPAAATAASKKFGSAALVGA VRKPVVPSVPM ASPAPGRLGAMSAAPSQNSQIRQNIRSLKEIL WK/RFLFFILFRVNDSDDLIMTENEVGKIALHIEK EMFNLQVTDN/RAYKSKYRSIMFNLKDPKNQG LFHRVLREEISLAKLVRLKPEELVSKELSTWKER PARSVMESRTKLHNESKKTAPRQEAIPDLEDSP VSDSEEQESARAVPEKSTAPLLDVFSMLKDTT SQHRAHLFDLNCICTGQVPSAEDEPAPKKQKLS ASVKKEDLKS KHDSSAPDPAPDSADEVMPEAVP EVASEPGLESASHPNVDRTYFPGPPGDGHPEPSPL EDLSPCPASCGSGVVTTVTVSGRDPRTAPSSSCT AVASAASRPDSTMVEARQDVPKPVLTSMVMPK SILAKPSSSPDPRYLSVPPSPNISTSESRSPPGDDT LFLSRLSTIWKGFINMQSVAKFVTKAYPVSGCFD YLSEDLPTIHIGGRIAPKTVWDYVGKLKSSVSK ELCLIRFHPATEEEEEVAYISLYSYFSSRGRFGVVA NNNRHVKDLYLPLSAQDPVPSKLLPFEGPGKRR LSGWR
3866	A	2	3181	AQQPVGRRGGASGAGGGRRGTTPRAGAGPGF QVSSGGCRLSKMRRFLRPGHDPVRERLKRDLFQ FNKTVEHGFPHQPSALGYSPSLRILAIGTRSGAIK LYGAPGVFEFMGLHQENNAVTQIHLPGQCQLVT LLDDNSLHLWSLKVKKGASELQEDSFTRGPP GAAPSATQITVVLPHSSCELLYLGTESGNVFVVQ LPAFRALEDRTISSDAVLQRLPEEARHRRVFEMV EALQEHPDPNQILIGYSRGLVVIWDLQGSRVLY HFLSSQLENIWWQRDGRLLVSCHSDGSYCQWP VSSEAQQPEPLRSLVPYGPFPCKAITRILWLTRQ GLPFTIFQGGMPRASYGDRHCISVIHDGQQTAFD FTSRVIGFTVLTEADPAATFDDPYALVVLAEEL VVIDLQTAGWPPVQLPYLASLHCSAITCSHHVSN IPLKLWERIIAAGSRQNAHFSTMEWPIDGGTSLTP APPQRDLLLLTGHEGTVRFWDASGVCLRLLYKL STVRVFLTDTDPNENLSAQGEDEWPPLRKVGSF DPYSDDPRLGIQKIFLCKYSGYLAVAGTAGQVLV LELNDEAAEQAVEQVEADLLQDQEGYRWKGHE RLAARSGPVRFEFGFPFVLVQCQPPAVVTSAL HSEWRLVAFGTSHGFLFDHQRRQVFVKCTLH PSDQLALEGPLSRVKSLLKSLRQSFRMRMRSRVS SRKRHPAGPPGEAQEGSAKAERPGLQNMELAPV QRKIEARSAEDSFTGFVRTLYFADTYLKDSSRHC PSLWAGTNGGTIYAFSLRVPPAERRMDEPVRAE QAKEIQLMHRAPVVGILVLDGHSVPLPEPLEVAH DLSKSPDMQGSQQLLVVSEEQFKVFTLPKVS AK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LKLLKLTALGSRVRRVSVAHFGSRRRAEDYGEHH LAVLTNLGDIQVVSLPLLKPQVRYSCIRREDVSGI ASCVFTKYGGFYLIISPSEFERFSLSTKGLVEPRC LVDSAETKNHRPGNGAGPKKAPSRARNSGTQSD GEEKQPGLVMERALLSDERAATGVHIEPPWGA ASAMAEQSEWLSVQAAR
3867	A	2	3181	AQQPVGRRGGASGAGGGRRGTTPRPRAGAGPGF QVSSGGCRLSKMRRFLRPGHDPVRERLKRDLFQ FNKTVEHGPHQPSALGYSPSLRILAIGTRSGAIK LYGAPGVFEFMGLHQENNAVTQIHLLPGQCQLVT LLDDNSLHLWSLKVKGGASELQEDESFTLRGPP GAAPSATQITVVLPHSSCELLYLGTESGNVFFVQ LPAFRALEDRTISSDAVLQRLPEEARHRRVFEMV EALQEHPRDPNQILIGYSRGLVVIWDLQGSRLVY HFLSSQQLENIWWQRDGRLLVSCHSDGSYCQWP VSSEAQQPEPLRSLVPYPFPCKAITRILWLTTRQ GLPFTIFQGGMPRASYGDRHCISVIHDGQQTAFD FTSRVIGFTVLTEADPAATFDDPYALVVLAEEL VVIDLQTAGWPPVQLPYLASLHCSAITCSHHVSN IPLKLWERIIAAGSRQNAHFSTMEWPIDGGTSLTP APPQRDLLLLTGHDGTVRFWDASGVCLRLLYKL STVRVFLTDTPNENLSAQGEDEWPPLRKVGSF DPYSDDPRLGIQKIFLCKYSGYLA VAGTAGQVLV LELNDEAAEQAVEQVEADLLQDQEGYRWKGHE RLAARSGPVRFEFGFPFVLVQCQPPAVVTSAL HSEWRLVAFGTSHGFLFDHQRRQVFVKCTLH PSDQLALEGPLSRVKSLSKSLRQSFRRMRRSRVS SRKRHPAGPPGEAQEGSAKAERPGLQNMELAPV QRKIEARSAEDSFTGFVRTLYFADTYLKDSSRHC PSLWAGTNGGTIYAFSLRVPPAERRMDEPVRAE QAKEIQLMHRAPVVGILVLDGHSVPLPEPLEVAH DLSKSPDMQGS HQLLV VSEEQFKVFTLPKVS AK LKLLKLTALGSRVRRVSVAHFGSRRRAEDYGEHH LAVLTNLGDIQVVSLPLLKPQVRYSCIRREDVSGI ASCVFTKYGGFYLIISPSEFERFSLSTKGLVEPRC LVDSAETKNHRPGNGAGPKKAPSRARNSGTQSD GEEKQPGLVMERALLSDERAATGVHIEPPWGA ASAMAEQSEWLSVQAAR
3868	A	1	2497	GDSSGGLVCEEPSGRFFLAGIVSWGICAEARRP GVYARVTRLRDWILEATTKASMPAPTMAPAPA APSTAWPTSPESPVVSTPTKSMQALSTVPLDWVT VPKLQECGARPAMEKPTRVVGFGAASGEVPW QVSLKEGSRHFCGATVVGDRWLLSAHCFNHT KVEQVRAHLGTASLLGLGGSPVKIGLRVVLHP LYNPGILDFDLAVLELASPLAFNKYIQPVCLPLAI QKFPVGRKCMISGWGNTQEGNATKPELLQKASV GIDOKTCSVLYNFSLTDRMICAGFLEGKVDSCQ VSGIKALYESELADARRVLDETARERARLQIEIG KLRAELDEVNKS AKKREGELTVAQGRVKDLES FHRSEVELAAALS DKGLES DVAELRAQLAKAE DGHA VAKKQLEKETLMRVDLENRCQSLQEELDF RKSVFEEEVRETRRRHERRLVEVDSSRQQEYDFK MAQALEELRSQHDEQVRLYKLELEQTYQAKLDS AKLSSDQNDKAASAAAREELKEARMRLESLSYQL SGLQKQASAAEDRIRELEEAMAGERDKFRKMLD

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				AKEQEMTEMRDVMQQQLAEYQELLDVKLALD MEINA YRKLLEGEERLKLSPSPSSRVTVSRATSS SSGSLSATGRLGRSKRKRWWRSPWQRPKRP HGHGWQRWLP PGPAGLGLGQR/HIEEIDLEGKFV QLKNSDKDQSLGNWRIKRQVLEGEELAYKFTP KYILRAGQMVTVWAAGAGVAHSPSTLVWKGQ SSWGTGESFRTVLVNADGEEVAMRTVKKSSVM RENENGE EEEEEAEFGEDLFHQGGDPRTTSRG YVM
3869	A	1	1942	RYRAGIPGDGRKDYIRLTPGLTLPGRAMFARG RRRRSGRAPPEAEDPDRGQPCNSCREQCPGFLH GWRKICQHCKCPREEHA VHA VPVDLERIMCRLIS DFQRHSISDDSGCASEEYAWVPPGLKPEQVYQ FFSCLPEDKVPYVNSPGEKYRIKQLLHQLPPHDS EAQYCTAL/EE/EEKKELRAFSQQRKRENLG/RLG IVRIFPVITIGAI/CEECGKQIGGGDIAVFASRASL GLLLGQPSCFVCTTCQELLVDLIYFYHVGKVYC GRHHAELRPRCQACDEIIFSPPECTAEGRHWHM DHFCCFECEASLGGQRYVMRQSRPHCCACYE HAEYCDGCGEHIGLDQGQMA YEGQHWASDR FCCSRCGRALLGRPFLPRRGLIFCSRACSLGSEPT APGPSRRWSAGPVTA PLAASTASFS AVKGASET TTKGTSTELAPATGPEEPSRFLRGAPHRHSMPEL GLRSVPEPPESPQPNLRPDDSAFGRQSTPRVSF RDPLVSEGGPRRTLSAPPAQRPRRSPPPRAPSRR RHHHHNHHHHNHRHPSRRRHYQCDAGSGSDSE SCSSPSSSSSESEDGFFLGERIPLPPLCRPMP AQDTAMETFNPSLSLPRDSRAGMPRQARDKNC IVA
3870	A	2	3485	FVWRVFYVHASCMPPRARSWEGAHA PVGMHV AEAHA CSSQQQMPPAQFWMLEWLLHLC AFLS TPSFPHWCCSNPHGSIADKPEEIVPASKPSRAAE NMAVEPRVATIKQRPSSRCFPAGSDMNSVYERQ GLAVMTPTVPGSPKAPFLGIPRGTMRRQKSIDSRI FLSGITEERQFLAPMLKFTRLSMPDTS EDIPPP PQSVPPSPPPSPPTTYNCPKSPTPRVYGTIKPAFNQ NSAAKVSPATRSDTVATMMREKGM YFRRELD YSLDSEDLYSRNGPQANFRNKRGM PENPYSE VGKIASKA VYVPAKPARRKGM LVKQSNVEDSPE KTCSIPIITIIVKEPSTSSSGKSSQGSSMEIDPQAPE PPSQLRPDESLTVSSPFAAAIAGA VRDREKRLEA RRNSPAFLSADLGDEHVGLGPPAPRTRPSMFPEE GDFADEDSAEQLSSPMPSATPREPENHFVGGAE SAPGEAGRPLNSTSKAQGPSSPAVPSASSGTAG PGNYVHPLTGRLLDPSSPLALALSARDRAMKES QQGPKGEAPKADLNKPLYIDTKMRPSLDAGFPT VTRQNTRGPLRRQETENKYETDLGRDRKGDDK KNMLIDIMDTSQKSAGLLMVHTVDATKLDNA LQEEDEKAEVEMKPDSSPSEVPEGVSETEGALQI SAAPEPTTVPGRTIVAVGSMEEAVILPFRIPPPPLA SVDLDEDFIFTEPLPPPLEFANSFDIPDDRAASVPA LSDLVKQKKSDTPQSPSLNSSQPTNSADSKKPAS LSNCLPASFLPPESFDAVADSGIEEVDSRSSSDH HLETTSTISTVSSISTLSSEGGENVDTCTVYADGQ AFMVDKPPVPPKPKMKPIHKSNALYQDALVEE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DVDSFVIPPPAPPPPGSAQPGMAKVLQPRTSKL WGDVTEIKSPILSGPKANVISELNSILQQMNREKL AKPGEGLDSPMGAKSASLAPRSPEIMSTISGTRST TVTFTVRPGTSQPITLQSRPPDYESTSGTRRAP PVVSPTEMNKETLPAPLSAATASPSALSDVFSLP SQPPSGDLFGLNPAGRSRSPSPSILQQPISNKPFTT KPVHLWTKPDVADWLESLNLGEHKEAFMDNEI DGSHLPNLQKEDLIDLVTRVGHMNIERALKQ LLDR
3871	A	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNLLTLDVKK KIKEVTEEVANKVSCAMTDEICRLSVLVDFECSE FHPNPDVLKIYKSELNKHIEDGMGRNLADRCTD EVNALVLQTQQEIIENLKPLLPAQIQDKLHTLIPC KKFDLSYNLNYHKLCSDFQEDIVFRFSLGWSSLV HRFLGPRNAQRVLLGLSEPIFQLPRSLASTPTAPT TPATPDNASQEELMITLVTGLASVTSRTSMGIIV GGVIWKTIGWKLLSVSLTMYGALYLYERLSWTT HAKERAFKQQFVNYATEKLRMIVSSTSANCSTHQ VKQQIATTFARLCQQVDITQKQLEEEIARLPKEID QLEKIQNNSKLLRNKAVQLENELNFTKQFLPSS NEES
3872	A	35	1171	VESRSAWHEGEDQIDRLDFIRNQMNLLTLDVKK KIKEVTEEVANKVSCAMTDEICRLSVLVDFECSE FHPNPDVLKIYKSELNKHIEDGMGRNLADRCTD EVNALVLQTQQEIIENLKPLLPAQIQDKLHTLIPC KKFDLSYNLNYHKLCSDFQEDIVFRFSLGWSSLV HRFLGPRNAQRVLLGLSEPIFQLPRSLASTPTAPT TPATPDNASQEELMITLVTGLASVTSRTSMGIIV GGVIWKTIGWKLLSVSLTMYGALYLYERLSWTT HAKERAFKQQFVNYATEKLRMIVSSTSANCSTHQ VKQQIATTFARLCQQVDITQKQLEEEIARLPKEID QLEKIQNNSKLLRNKAVQLENELNFTKQFLPSS NEES
3873	A	2944	2089	PVCTALTPGRMTDDKDVLRDVWFGRIPTCFTLY QDEITEREAEPYLLPRVSYLTIVTDKVKKHQ KVMRQEDISEIWFYEGTPLKWHYPIGLLFDLLA SSSALPWNITVHFKSFPEKDLLHCPKDAIEAHF MSCMKEADALKHKSQVINEMQKKDHKQLWMG LQNDRFDQFWAINRKLMEYPAEENGFRYPFRY QTTTERPFIQKLFPRVAADGQLHTLGDLLKEVCP SAIDPEDGEKKNQVMHIGIEPMLTPLQWLSEHL SYPDNFLHISIPQPTD
3874	A	776	366	QARGAPSSPMCPPLPLAAAVAAPRAPRLRLNRG LAAAMSTAQSLKSDYEVFGRVQGVCFRMYTE DEARKIGVVGWVKNTSKGTVTGQVQGPEDKVN SMKSWLSKVGSPSSRIDRTNFSNEKTISKLEYSNF SIRY
3875	A	1081	182	SLSSCQTDPRPMSAPLDAALHALQEEQARLKMR LWDLQQLRKELGDSPKDKVPFVVKIPLVFRGHT QQDPEVPKSLVSNLRIHCPLLAGSALITFDDPKVA EQVLQKQKHTINMEECRRLRVQVQPLELPMVTTIQ VMVSSQLSGRRVLVTGFPASRLRLSEEELLDKLEIF FGKTRNGGGDVDVRELLPGSVMLGFARDGVAQ RLCQIGQFTVPLGGQVPLRVSPYVNGEIQA RSQPVPRSVLVLPDILDGPELHDVLEIHFQKPT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				RGGGEVEALTVVPQQQGLAVFTSESG
3876	A	26	431	RMMKCPQALLAIFWLLSWVSSSEDKVVQSPLSL VVHEGDTVTLNCSYEVTNFRSLLWYKQEKKAPT FLFMLTSSGIEKKSGRLSSILDKKELSSILNITATQ TGDSAIYLCAVEAQCSLVTCSLYNSTAEALQL
3877	A	3	1291	KAFLRLAERGAAAAMLWSGCRRFGARLGCLPG GLRVLVQTGHRSLTSCIDPSMGLNEEQKEFQKV AFDFAAREMAPNMAEWDQKELFPVDVMRKA QLGFGGVYIQTDTVGGSGLSRLDTSVIFEALATGC TSTTAIYISIHNMCAWMIDSFGNEEQRHKFCPLC TMEKFASYCLTEPGSGSDAASLLTSAKKQGDHYI LNGSKAFISGAGESDIYVVMCRTGGPGPKGISCIV VEKGTPLSFGKKEKKVGWNSQPTRAVIDECA VPVANRIGSEGQGFLLAVRGLNGGRINIASCGLA AHASVILTRDHLNVRKQFGEPLASNOYLQFTLA DMATRLVAARLMVRNAVALQEERKDAVALCS MAKLFA TDECFAICNQALQMHHGGYGLKDYAV QQYVRDSRVHQILEGSNEVMRILISRLQ
3878	A	10	1014	LPGSTISSSGCQAPGRADSSGGARNSRRGDSRPG SCNRQAVAPPCPSGPGQSRHWIHRGTAPQAGETR TLGRGSSAPNACSASVTPCCPSSPPS*SCL*PTRRS PQNSSSTEYVRGFQWHLPLST**PFSS*QWPGQH TQGCCKLLGKQTTHLPCSTWPA**PSPSCLTRFR* W*PSLMCLWASSCSVCV*SPSGSCRH*LWGTHST SRTC*ARRSSALPTGLCTDDTSWASSSKARPCAL QRPSLSSLSPLCTC*W*LSSSPMSARSAPGAET GSWATGSPRLTQWKSRLTSTSHSARSAWKPSA TESTPSWPRFSSWTSGEDPASPAPAI
3879	A	200	699	LLLTGYIQTQLNQQLSGNQEMQAVDNLTSAPG NTSLCTRDYKITQVLFPLLYTVLFFVGLITNGLA MRIFFQIRSKSNFIIFLKNTVISDLLMLTFPFKILS DAKLGTPRLTFVCQVTSVIFYFTMYISISFLGLIT IDRYQKTTRPFKTSNPKNLLGAKILK
3880	A	26	169	QPETDTMVHLTPEEKSAVTALWGKVNVEDAG DDLCOQLVDRPLRI
3881	A	37	1100	TPLDFWPGFVLSWLQPLSASLRARRAASGPAC RIMPTTVDDVLEHGGEFFQKQMFLLALLSAT FAPIYVGIVFLGFTPDHRCRSPGVAELSLRCGWSP AEELNYTVPGPGPAGEASPRQCRRYEVDWNQST FDCVDPLASLDTNRSRLPLGPCRDGWVYETPGSS IVTEFNLVCANSWMLDLFQSSVNVGFFIGSMSIG YIADRFGRLCLLTTVLINAAAGVLMASPTYTW MLIFRLIQGLVSKAGWLIGYLITEFVGRRYRRTV GIFYQVAYTVGLLVLAGVAYALPHWRWLQFTV ALPNFFFLYYWCIPESPRWLISQNKNAEAMRIK HIAKKNGKSLPASL
3882	A	573	1620	KSKCRFPEGLSEGFGPMRKEALSSGSVQEA LDEPQEQAEGLTVYVISEHSSLLPQDMMSYIGP KRTAVVRGIMHREAFNIIGRRIVQVAQAMSLTED VLAAALADHLPEDKWSAEKRRPLKSSLGYEITFS LLNPDPKSHDVYWDIEGAVRRYVQPFNLALGAA GNFSVDSQILYYAMLGVNPRFDSASSSYLDMMH SLPHVINPVESRLGSSAASLYPVLNFLLYVPELAH SPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDS KTYNASVLPVRVEVDMVRVMEVFLAQLRLFLGI

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				AQPQLPPKCLLSGPTSEGLMTWELDRLLWARSV ENLATATTTTSLA
3883	A	2369	844	RIHREEDFQFILKGIARLLSNPLLQTYLPNSTKKIQ FHQELLVLFWKLCDFNKVGGPRGALQGDGEQLP Q*PGGRDSVRLRGVQSCPSLELSPLGPSHP*KF LFFVLKSSDVLVDILVPILFFLNDARADQSRVGLM HIGVFILLLLSGECNFGVRLNKPYSIRVPM DIPVF TGTHADLLIVVFHKIITSGHQRLQPLFDCLLTIVV NVSPYLKSLSMVTANKLLHLEAFSTTWLFSAA QNHHLVFFLLEVFNIIQYQFDGNSNLVYAIIRKR SIFHQLANLPTDPPTIHKALQRRRTPEPLSRTGS QGGAPPWRAPAPLPLQSQAPSRPVWLLQALTS *PRSPRCQRMAPCGPWNLSPSRAWMAARLRGS PARHGGSSGDRP/HSSASGQWSPTEWVLSWKS KLPLQTIMRLLQVLVPQVEKICIDKGLTDESEILR FLQHGTLVGLLPVPHILIRKYQANS GTAMWFRT YMWGVIYLRNVDPVWYD TDVKLFEIQRV
3884	A	1	804	NGPRAPFSQEGQSTGPPPLIPRLGQHGAQGRIPPL NPGQGPGPNKDDSRGPPNHMGPMSEERRHEQSG GPEHGPERGRLRGQDCRGPPDRRGPHDPDFDDF SRPDDFHPDKRFGHRLREFEGRGGPLPQEEKWR RGGPGPPFPDHPREFSEGDRGAARGPPGA WEG RRPGG*TFPPGSRGPTFS/SGAEESFRRGAPPRHE GRAPPRGRDGFPGPEDFGPEENFDASEEAARGRD LRGRGRGTPRGERVTKDTWSGRIGCRIHWL
3885	A	3	996	GRRRAGPAHSARMYNMME TELKPPGPQQTSGG GGNSTAAAAGGNQKNSPDRVKRPMNAFMVW SRGQRRKMAQENPKMHNSEISKRLGAEWKLLSE TEKRPFIDEAKRLRALHMKEHPDYKYRPRRKT TLMKKDKYTLPGGLLAPGGNSMASGVGVGAGL GAGVNQRMDSYAHMNGWSNGSYSMMQDQLG YPQHPGLNAHGAAQM QPMHRYDVSALQYNM TSSQTYMNG/SRPTYSMSYSQQGTPGMAPGS/MG SVVKSEASSPPVVTSSSHSRAPCQAGDLRDMIS MYLPGA EVPEPAAPSRLHMSQHYQSGVPVGTAI NGTLPLSHM
3886	A	773	317	QCTQKAAEGYTQFYVVDVLDGKLACVNKCTKG TKSQMNCNLGTCQLQRSGPRCLCPNTNTHWYW GETCEFNIKSLVYGIVGAVMAVLLLALILILFS LSQ/RKRHRPESEGEADFGLENA TNNGPTLET VDSGTELHIQRP EMVASTV
3887	A	3	466	VD FRVKTLLVDNCFVLQLWDTAGQERYHSMT RQLLRKADGVVLMYDITSQESFAHVRYWLDCL QDAGSDGVVILLGNKMDCEEERQVSVEAGQQL AQELGVYFGCSAALGHNILEPVVNLARSLRMQ EEGLKDSL VKVAPKRPPKRFGCCS
3888	A	3412	3144	QNIDITNFSSSWNDGLAFCALLHTYLP AHIPYQEL NSQDKRRNFMLAFQAAESVGIKSTLDINEMVRT ERP DWQNVMLYVTAIYKYFET
3889	A	1	1160	LVVTAITAILAFPNEYTRMSTSELISELFNDCGLL DSSKLC DYENR FNSTKGGELPDRPAGVG VYSAM WQLALTILKIVITIFTGMKIPSGLFIPSMAGAI AGRLLGVGMEQLAYYHQEWTVFNSWCSQGAD CITPGLYAMVGAAACGGVTRMTVSLVVMFEL TGLEYIVPLMAAAMTSKWVADALGREGIYDA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				HIRLNGYPFLEAKEEF AHKTLAMDVMKPRRNDP LLTVLTQDSMTVEDVETISETTYSGFVVVSRES QRLVGFVLRRLIISIENARKKQDGVVSTSHYFTE HSPPLPPYTPPTLKLRLNLDLSPFTVTDLTPMEIVV DIFRKLGLRQCLVTHNGRLLGIITKKDVLKHIAQ MANQDPDSILFN
3890	A	1	387	SWCWTGIFVLGTTNLRLEGSWYRSLWGPFGNTT TATLGFAGAPQAPVGDVALNQPDMCVYRRGRKK RVPTYTKLQLKELENEYAINKFINKDKRRRISAAT NLSEQRQVTIWFQNRVRVKDKKIVSKLKDTV
3891	A	2	2914	RGGGGDHKMA DLSLLQEDLQEDADGFGVDDYS SESDVIIIPALDLAST/QDEMVERPLGR/LDK/YA ASENH*PDKMVAPEFASIPLE/VCDDEDCIAV LGKN*PDWADDSEPT/VRAAELEQVPHIALFLFK KTRL SITICFFSKFLPYCGLD TLADQN/NQVRKT SQAALL\ALLEQELIERFDVETKVCPLIELTAPDS NDDVKTEA VAIMCKMAPMVGKDITERLILPRFC EMCCDCRMFHVVRK/VCAANFGDICSVVGQQAT EEMLLPRFFQLCSDNVWGVKACAE CFMAVSC ATCQEIRRTKLSALFINLISDPSRWVRQA AFQSLG PFISTFANPSSSGQYFKESKSSEEMSVENNRTR DQEAPEDVQVRPEDTPSDLSVSNSSVILENTMED HAAEASGKPLGEISVPLDSSLLCTLSSESHQEAAS NENDKKPGNYKSMRLPEVGTTSQDSALLDQELY NSFHFWRTPLEIDL DIELEQNSGGKPSPEGPEEE SEGPVPSSPNITMATRKELEEMENLEPHIDDPDV KAQVEVLSAALRASSLDAHEETISIEKRSDLQDE LDINELPNCKINQEDSVPLISDAVENMDSTLHYIH NDSDSLNNSSFSPDEERRTKVQDVVPQALLDQY LSMTDPSRAQTVDTEIAKHCAYS LPGVALTLGR QNWHLCLRETYETLASDMQWKVVRTLA FSIHELA VILGD\QLTAADLVPIFNGFLK*PSMKSRIGVLKH LHDFLKLLHIDKRREYL YQLQEFVTDNSRNWR FRAELAEQLILLELYSPRDVYDYLRIALNLCAD KVSSVRWISYKLVSEMVKKLHAATPPTFGVDLIN ELVENFGRCPKWSGRQAFVFCQTVIEDDCLPM DQFAVHLMPHLLTLANDRVPNVRVLLAKTLRQT LLEKDYFLASASCHQEA VEQTIMALQMDRDSDV KYFASIH PASTKISEDAMSTASSTY
3892	A	158	2191	VPLPAPSGLSGGGSRGAGCKKAPPGRAPAPGLAP LRPSEPTMAVPPGHGPFSGFPGQEHTQVLPDVR LLPRRLPLAFRDATSA PLRKLSVDLIKTYKHINEV YYAKKKRRAQQAPPQDSSNKKEKKVLNHGYDD DNHDYIVRSGERWLEREIDSLIGKGSFGQVVK A YDHQTQELVAIKIKNKKAFLNQAQIELRLLELM NQHDTEMKYYIVHLKRHFMRNHLCLVFELLS YNLYDLLRNTHFRGVSLNLTRKLAQQLCTALLF LATPELSIIHCDLKPENILL CNPKRSAIKIVDFGSS CQLGQRIYQYIQSRFYRSPEVLLGTPYDLAIDMW SLGCILVEMHTGEPLFGSGSNEVCPQEGVDQMNRI VEVLGIPPAAML DQAPKARKYFERLPGGGWTLR RTKELRKDYQGGPTRRLQEV LGVQTGGPGGRR A GEPGHSPAD\YLRFQDLVLRMLEYEPAA RISPLG ALQHGGFFRRTADEATNTGPAGSSASTSPAPL DTC PSSSTASSISSSGSSGSSSDNRTYRYSNRYCGGP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				GPPITDCEMNSPQVPPSQPLRPWAGGDVPHKTH QAPASASSLPGTGAQLPPQPRYLGRPPSPTSPPPP ELMDVSLVGGPADCSPPHPAPAPQHPAASALRT RMTGGRPPLPPPDDPATLGPLHLGLRGVPGSTAAS S
3893	A	68	258	PEEYYPFSPTLQQLFFFLDSDMGSRPESMGCRK NTVPRPASPTAGTDPQTFLHTWVSECRD
3894	A	1120	136	SLPLAPAPAVAGPVALCPAGLCPAQPGMPAGPA AASGSHPEVGSVLQRSSQPHWPNPWPGAGHLP PAGFPFYNPPAGPGAAAGLA*SPPRSSPTPCSVGP QSCPANASAPPAQPCLAGAPPAASLPPPGPGSVS AAPAGGGPAPAEPPLGVPPVPAWLLPDSPLPGT HSGPPPAAVSLPPAAAACPVVPPPLPHPPDLES PSAAAPNPGCAGGIRHFPFGSPEASSPLRPAAAPA LLPLRPPS*P/VPWKPLHSPVAVAGGSFVAGGSV LPAPDLQPRPSGPPAASPTPGPGVAQPPPGSAVL PTVP*APPVSGAAPGRKREW
3895	A	2	1347	FGAVSYRPGNGSCWVKVTASSDLSLISCLCPR SLCSSQACVLPVPGPSLLLPQGLHVGCSAGTRW PLSCSIDFQRLLAHEEETQKRRAKESGMAFTQLT FRDVAIEFSQDEWKCLNSTQRTL YRDVMLENYR NLVSLDLRNCVIKELAPQQEGNP/ARSIPHSDIGT T*KT*H*RVLLQGNQEKNTL*LSVER**KKLQQ SDYGPKRKSYL*ERPTR*KRYRKQVY*TSA*LSF LPHPHLQQAEGKIYECNHVEKSVNHGSSVSP PQIISSTIKTHVSNKYGTDFICSSLLTQEQKSCIRE KPYRYIECDKALNHGSHMTVRQVSHSGEKGYKC DLCKGVFSQKSNLARHWRVHTGEKPYKCNECD RSFSRNSCLALHRRVHTGEKPYKCYECDKVFSR NSCLALHQKTHIGEPYTCKEKGQAFSVRSTLTN HQVIHSDK
3896	A	202	498	MVQSCSAYGCKNRYDKDKPVSFHKFPLTRPSLC KEWEAAVRRKNFKPTKYSSICSEHFTPDCFKREC NNKLLKENAVPTIFLCTEPHDKKEDLLEPQEQ
3897	A	2	382	SHGLSRAPHLAAPAPALASRPCFSAPCSQGGG GGGPATMIHFILLFSRQGKLRLOK WYITLPDKER KKITREIVQILSRGHRTSSFVDWKELKLVYKRYA SLYFCCAIE/NQDNELLTLENVHR
3898	A	718	305	SEQEPLLDTPGSRWDILETEEHYKSRWRSIRIL YLTMFLSSVGFVVMMSIWPYLQKIDPTADTSFL GWVIASYSLGQMVASPIFGLWSNYRPRKEPLIVSI LISVAANCLYAYLHIPASHNKYYMLVARGLLGIG
3899	A	24	718	FRGRPGIPEREKGKGNHSFVEVARVIVVDLHSRLG GAMAERKGTAKVDFLKKIEKEIQQKWDTERVFE VNASNLEKQTSKGKYFVTFPPYPMNGRLHLGHT FSLSKCEFAVG YQRLKGKCCFLPFGLHCTGMPIK ACADKLKREIELY/GCPPDFPDEEEEEETS VKTE DIIHKDKAKGKSKAA/AKAGSSKYQWGMKSLG LSDEEIVKFSEAEHWLDYFNALAIQDLKRMG
3900	A	360	1	VPATSSNVSPSSSESSEPDLSRSSSSDAPSSSPSV SPCSLSLSSPESPLPTLLSSKSPAGSAGPTCGCPS GGLRATA/PSRLSSSIAAH/SSAPETSRPAAARE RSPPLHDRESHE
3901	A	193	345	GEWAVPPAPGGQGVSIHPGPEPGQSGSVHIAPRQ GEGSDRTEPLICPKAAP

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3902	A	1188	1389	NPAARSAAREGSPALPPPPVS/SSSGLGLLPLSP PGSHAANPALSPRAPHSHYRPRRCGPRRRPR
3903	A	63	396	NNMRNPHLSSNHYLNARTETVFARMESVKQRI LAPGKEGLKNFAGKSLGQIYRVLEKKQDTGETIE LTEDGKPL*VPERKAPLCDCTCFGLPRRYIAIMS GLGFCISFG
3904	A	732	1046	AMSECPLILYIHKHIDTYSQSYLFNDLFYPVYSGG RMVTYEHLEVVFGKSEDEHYPLW*VLF GK*YA VAPNALMFIRFM*NCTFVPKLP*VMDLK**LQYK SR
3905	A	46	910	QPPPPPPPPSPPPPPFPARALSHLRHPDACLFPS PFPLPCSTMPGMMMEKGPELLGKNRSANGSAKSP AGGGGSGASSTNGGLHYSEPESEGCSSDDEHDVG MRVGAEYQARIPEFDPGATKYTDKNDGGMLVW SPYHSIPDAKLDEYIAIAKEKHGYNVEQALGMLF WHKHNIKSLADLPNFTFPDEWTVEDKVLFEQ AFSFGKSFHRIQQMLPDKTIASLVKYYYSWKK TRSRTSLMDRQARKLANRHNQGDSDDDVEETHP MDGNSDYDPKKEAKKEGMS
3906	A	2	513	KVCNCCSQELETSTFTYVDKNINLEQRNRSSPSAK GHNHPGELGWENPNEWSQEAALISEEEDDTSS EATSSGKSIDYGFISAILFLVTGILLVIISYIVPREV TVDPNTVAAREMERLEKESARLGAHLDRCVIAG LCLLTGGVILSCLLMMSMWKGELYRRNRFAS
3907	A	71	412	ILIMSNCLQNFLKITSTRLLCSRLCQQLRSKRKFF GTVPISRLHRRVVITGIGLVTPLVGTHLVWDRLI GGESGIVSLVGEEYKSIPCSVAAYVPRGSDEGQF NEQNFVSKSD
3908	A	77	746	LGTLGWRAPLFSRCLAFHSPFILLNTPKLVKTAE LPPDRNYVLGAHPHGIMCTGFLCNFSTESNGFSQ LFPGLRPWLAVLAGLFYLPVYRDYIMSFGLCPVS RQSLDFILSQPLGQAVVIMVGGAEALYSVPGE HCLTLQKRKGFRVRLALRHGASLPVYVSFGENDIF RLKAFATGSWQHWQCLTFKKLMGFSPCIFWGR GLFSATSWGLLPFAVPITTV
3909	A	1	793	FRAAGRPAAAMGDIPVVLSSWKASPGKVTEAV KEAIDAGYRHFDCAFYHNEREVGAGIRCKIKE GAVRREDLLIATKLWCTCHKKSLVETACRKSILK ALKLNYLDLYLIHWPMGFKPPHPWIMSCSELSF CLSHPRVQDLPLDESNMVIPSDTDFLDTWEAME DLVITGLVKNIGVSNNFHEQLERLLNKPGLRFPK LTNQIECHPYLTQKNLISFCQSRDVSVTAYRPLG GSCEGVDLIDNPVIKRIAKEHGKSPAQILI
3910	A	202	705	FFTMRKKVDNRIRILIENGVAERQSRSLFVVVG RGKDQVVLHMLSKATVKARPSVLWCYKKEL GFSSHRKKRMRQLQKKIKNGTLNIKQDDPFELFI AATNIRYCYNETHKILGNTFGMCVLQDFEALTP NLLARTVETVEGGGLVVILLRTMNSLKQLYTVT M
3911	A	3	723	AGRGARAAGEGGGPFKSRPRPLPSSRSLPAVGGG RYGADKMAAGGAVAAAPCECRLLPYALHKWSSF SSTYLPENILVDKPNQSSRWSSSESNYPQYLILK LERPAIVQNITFGKYETHVCNLKKFKVFGGMN EENMTELLSSGLKNDYNKETFTLKHKIDEQMFP RFIKIVPLLSWGPFNF SIWYVELSGIDDPDIVQPC

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				LNWYSKYREQEAIRLCLKHFRQHNYTEAFESLQ KKT
3912	A	2	461	FEKKQLRRPSLFLLGCCSFGIMAPSLWKGLEGIG LFALAHAAFSAAQHRSYMRLTEKEDESLPIDIVL QTLFAFVTCYGIVHIAGEFKDMDATSELKNKTF DTVRNHPSFYVFNHRGSEYFSGPSDTANSSNQDA LSSNTSLKLRKLESLRR
3913	A	362	20	APGRPEAKVPERSRESGSRVRGPLLQLRPGRTS RPASGRGRGGAGGSYGKMRKPD SKIVLLGDMN VGKTSLLQRYMERRFPD TVSTVGGAFYLKQWRS YNISIWDTAGEAGAA
3914	A	1	7545	PGIRVGITSQTGLSSNLQENCSKLAFISSHGTEKQ LQCMPEGRGRASSISDLQGGKFEKGTGEKHV PGVGSARHSPQASAGGSPWQRGKAQTRWLGP DPGRKRRRGSPQEEGGLRVSAARLLCSGANRC KVLVRQNSTPNTQQPAVHPSTPPSRPLPQAGRCL VAPLRPHPDWVAAKTLAKALRAPGKPWRLAAP SPLGDLGAPGLPGPSTAPRTLSVEEPGVECNQLC LYADVTDPVLC LGQKDPGVEGKHCEKEKISSSK ELKHVHAKSEPSKPARRLSESLHVVDENKNESKI EREHKRRTSTP VIMEGVQEETDTRDVKRQVERSE ICTEEPQKQKSTLKNKHLKKDDSETPHLKSLK KEVKSSKEKPEREKT SEDKLSVKHKYKGDCMH KTGDETELHSSEKGLKVEENIQKQSQQTKLSSDD KTERKSKHRNERKLSVLGKDGPVSEYIIKTDEN VRKENNKKERRLSAEKTKAEHKSRRSSDSKIQK DSLGSKQHGITLQRRSESYSEDKCDMDSTNMD NLKPEEVVHKEKRRRTKSLLEEKLVLSKSKTQG KQVKV VETELQEGATKQATTPKPDKEKNTEEND SEKQRKSKVEDKPFEE TGVEPVLETASSAHSTQ KDSSHRAKLPLAKEKYKSDKDSTSTRLERKLSG GHKSRSLKHSSKDIKKK DENKSDDKD GKEVDSS HEKARGNSSLMKKLSRRLCENRRGSLSQEMAK GEEKLAANTLSTPSGSSLQRPKKS GDMTLIPEQEP MEIDSEPGVENVFEVSKTQDNRRNNNSHQDIDSEN MKQKTSATVQKDELRTCTADSKATAPAYKPGR GTGVNSNSEKHADHRSTLTKKMHIQSAVSKMNP GEKEPIHRGTTEVNIDSETVHRMLLSAPSEND RV QKNLKNATAEEHVAQG DATLEHSTNLDSSPSLSS VTVVPLRESYDPDVIPLFDKRTVLEGSTASTSPAD HSALPNQSLTVRESEVLKTSDSKEGEGFTVDTP AKASITSKRHIPEAHQATLLDGKQGVIMPLGSK LTGVIVENENITKEGGLVDMAKKENDLNAEPNL KQTIKATVENGKKDGIAVDHV VGLNTEKYAETV KLKHKRSPGKVKDISIDVERRNENSEVDT SAGS SAPSVLHQNRNGQTEDVATGPRRAEKTSVATSTE GKDKDVTLSPVKAGPATTTSETRQSEVALPCTS IEADEGLIIGTHSRNNPLHVGA EASECTVFAAAEE GGAVVTEGFAESETFLTSTKEGESGEC AVESED RAADLLAVHAVKIEANVNSV VTEEKDDAVTSAG SEEKCDGSLSRDSEIVEGTITFISEVESDGA VTSAG TEIRAGSISSEEDVGSQGNMMRMGP KKETEGTV TCTGAEGRSDNFVICSVTGAGPREERMVTGAGV VLGDNDA PPGTSASQEGDGSVNDGTEGESAVTS TGITEDGEGPASCTGSEDSSEGFAISSESEENGESA

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				<p>MDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKE EDEEGEDVVTSTGRGNEIGHASTCTGLGEESEGV LICESAEGDSQIGTVVEHVEAEAGAAIMNANENN VDSMSGTEKGSKDTCSSAKGIVESSVTSVSG KDEVTPVPGGCEGPM TSAASDQSDSQLEKVEDT TISTGLVGGSYDVLVSGEVPECEVAHTSPSEKED EDIITSVENEECDGLMATTASGDITNQNSLAGGK NQGKVLIISTTTNDYTPQVSAITDVEGGLSDALR TEENMEGTRVTTEFEAPMP SAVSGDDSQLTASR SEEKDECAMISTSIGEEFELPISSATTIKCAESLQP VAAA VEERATGPVLISTADFE GPMPSAPPEAES P LASTSKEEKDECALISTSIAEECEASVSGVVVESE NERAGTVMEEEKD GSGHIISTSSVEDCEGPVSSAVP QEEGDP SVTPAEEMGDTAMISTSTSEGCEAVMIG AVLQDEDRLTITRVEDLSDAIIISTSTAECMPISA SIDRHEENQLTADNPEGNGDLSATEVSKHKVPM PSLIAENNCRCPGPVRGGKEPGPVLAVSTEEGHN GPSVHKPSAGQGHPSAVCAEKEEKHGKECPEIGP FAGRGQKESTLHLINAEKNVLLNSLQKEDKSPE TG TAGGSSTASYSAGRGLEGNANSPAHLRGPEQ TSGQTAKDSSVSSIRYLAAVNTGAIKADDMPPVQ GTVAEHSFLPAEQGSEDNLKTSTTKCITGQESKI APSHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFPEEGDIMVTVSSE ENVCDIGNEESPLNVLGGLK LKANLKMEAYVPS EEEKNGEILAPPESLCGGKPSGIAELQREPLLVNE SLNVENS GFRTNEEIHSESYNKGEISSGRKDNAE AISGHSVEADPKVEVEEEERHMPKRKRKQHLYLSS DEPDDNPDVLDSRIETAQRQCPETEPHATKEENS RDLEELPKTSSETNSTTSRVMEEKDEYSSSETTGE KPEQNDDDTIKSQE</p>
3915	A	1	7545	<p>PGIRVGITSQTGLSSNLQENCSKLAFISSHGTEKQ LQCMPEGRGRASSISDLQKGFEKGTGEKHV PGVGSARHSPQASAGGSPWQRGKAQTRWLGP DPGRKRRRGSPQEEGGLRVSAARLLCSGANRC KVLVRQNSTPNTQOPAVHPSTPPSRPLPOAGRCL VAPLRPHPDWVAAKTLAKALRAPGKPWRLAAP SPLGDLGAPGLPGPSTAPRTLSVEEPGVECNQLC LYADVTDVPLCLGQKDPGVEGKHCEKEKISSSK ELKHVHAKSEPSKPARRLSESLHVVDENKNESKI EREHKRRTSTPVIMEGVQEETDTRDVKRQVERSE ICTEEPQKQKSTLKNKHLKDDSETPHLKSLK KEVKSSKEKPEREKTPSEDKLSVKHKYKGD CMH KTGDETELHSSEKGLKVEENIQKQSQQTKLSSDD KTERKSKHRNERKLSVLGKDGKPVSEYIKTDEN VRKENNKKERRLSAEKTAEHKSRRSSDSKIQK DSLGSKQHGITLQRRSESYSEDKCDMDSTNMDS NLKPEEVVHKEKRRTKSLLLEKLV LKSKSKTQG KQVKV VETELQEGATKQATTPKPDKEKNTEEND SEKQRKSKVEDKPFEETGVEPVLETASSAHSTQ KDSSHRAKLPLAKEKYKSDKDSSTRLERKLS GHKSRSLKHSSKDIKKDENKSDDKDGKEVDSS HEKARGNSSLMKKLSRRLCENRRGSLSQEMAK GEEKLAANTLSTPSGSSLQRPKKS GDMTLIPEQEP MEIDSEPGVENVFEVSKTQDNRNNNSHQDIDSEN</p>

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				MKQKTSATVQKDELRTCTADSKATAPAYKPGR GTGVNSNSEKHADHRSTLTCKMHQSAVSKMNP GEKEPIHRGTTEVNIDSETVHRMLLSAPSENDRV QKNLKNATAEEHVAQGDATLEHSTNLDSSPSLSS VTVVPLRESYDPDVIPLFDKRTVLEGSTASTSPAD HSALPNQSLTVRESEVLKTSDSKEGEGFTVDTP AKASITSKRHIPEAHQATLLDGKQGVIMPLGSK LTGVIVENENITKEGGLVDMAKKENDLNAEPNL KQTIKATVENGKKDGIADVHVGLNTEKYAETV KLKHKRSPGKVKDISIDVERRNENSEVDTSAGSG SAPSVLHQNRNGQTEDVATGPRRAEKTSVATSTE GKDKDVTLSPVKAGPATTTSSETRQSEVALPTS IEADEGLIIGTHSRNPLHVGAEESECTVFAAAEE GGAVVTEGFAESETFLTSTKEGESGECVAESED RAADLLAVHAVKIEANVNSVVTTEKDDAVTSAG SEEKCDGSLSRDSEIVEGTITFISEVESDGAVTSAG TEIRAGSISSEVDGSQGNMMRMGPKKETEGTV TCTGAEGRSDNFVICSVTGAGPREERMVTGAGV VLGDNDAPPGTSASQEGDGSVNDGTEGESAVTS TGITEDGEGPASCTGSEDSSEGFASSESEENGESA MDSTVAKEGTNVPLVAAGPCDDEGIVTSTGAKE EDEEGEDVVTSTGRGNEIGHASTCTGLGEESEGV LICESAEGDSQIGTVVEHVEAEAGAAIMNANENN VDSMSGTEKGSKDTDICSSAKGIVESSVTSVSG KDEVTPVPGGCEGPMTSAASDQSDSQLEKVEDT TISTGLVGGSYDVLVSGEVPECEVAHTSPSEKED EDIITSVENECDGLMATTASGDITNQNSLAGGK NQGVLIISTSTTNDYTPQVSAITDVEGGLSDALR TEENMEGTRVTTEFEAPMPSAVSGDDSQLTASR SEEKDECAMISTSIGEEFELPISSATTIKCAESLQP VAAAVEERATGPVLISTADFEQPMPSAPPEAESP LASTSKEEKDECALISTSIAEECEASVSGVVVESE NERAGTVMEEKDGSGIISTSSVEDCEGPVSSAVP QEEGDPVTPAEEMGDTAMISTSTSEGCEAVMIG AVLQDEDRLTITRVEDLSDAAIISTSTAECMPISA SIDRHEENQLTADNPEGNGDLSATEVSKHKVPM PSLIAENNCRCGPVVRGGKEPGPVLAVSTEEGHN GPSVHKPSAGQGHPSAVCAEKEEKHGKECPEIGP FAGRGQKESTLHLINAEKNVLLNSLQKEDKSPE TGTAGGSSTASYAGRGLEGNANSPAHLRGPEQ TSGQTAKDSSVSSIRYLAAVNTGAIKADDMPVQ GTVAEHSFLPAEQQSEDNLKTSTTKCITGQESKI APSHTMIPPATYSVALLAPKCEQDLTIKNDYSGK WTDQASAEKTGDDNSTRKSFEEGDIMVTVSSE ENVCDIGNEESPLNVLGGLKLANLKMEAYVPS EEEKNGEILAPPESLCGGKPSGIAELQREPLLNE SLNVENSGFRTNEEIHSESYNKGEISSGRKDNAE AISGHSVEADPKEVEEEERHMPKRKRKQHYLSSE DEPDDNPDVLDRIETAQRQCPETEPHATKEENS RDLEELPKTSSETNSTTSRVMEEKDEYSSSETTGE KPEQNDDDTIKSQE
3916	A	2	773	GPFGLVWPSAKPGPVTAVEARPPDASDPEGLRG GSPAPLLAPGPLDPSGRLHPAVSMMSYLKQPPYG MNGLGLAGPAMDLLHPSVGYPATPRKQRRERTT FTRSQLDVLEALFAKTRYPDIFMREEVALKINLPE

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SRVQVWFKNRRRAKCRQQQSGSGTKSRPAKKK SSPVRESSGSESSGQFTTPAVSSSASSSSASSSSA NPAAAAAAGLVVAKLPCPLHIFSLCVFIEENRLV SGSWARDIRSVEETDKSGYR
3917	A	2	776	RNIPGRRFRPPGLRRLKGPMPREPRGYRTRVP ALRELVPSSHAGSGASEHCQNNRQGSQRHRASR NVQAGGALAPPRHLCGLCSRLHFLKPDLSVRAA PSRAGASVMALRKELLKSIWYAFTALDVEKSGK VKSQRLRVLSHNLTYVLHIPHDPVALEEHRDDDD DGPVSSQGYMPYLNKYILDKVEEGAFVKEHFDE LCWTLTAKKNYRADSNNGNSMLSNQDAFRLWCL FNFLSEDKYPLIMDPDEGEYLLKRYR
3918	A	10	318	WQDLVCLGGSRAQEQKPLQQLWNAILLVAMLL CTGLVVQAQRQASRQSRELGGQVDLFKRRVV RRLASLKTTRCRLSRAAQGLPDPAETCAVCLD YFCNKQ
3919	A	1	204	RVLTAINHTLKENLRKFYKGGKDKPLDLRPKKT RAMRRRLNMHEENLTKKQHRKERLYPLRKYA AKA
3920	A	1	654	RCCRSFVAPLQEKVVFFGLFGLGAILCLSFSWLFHT VYCHSEGVSRFLSKLDYSGIALIMGSFVPWLYY SFYCNPPQCFIYLIVICVLGIAIIVSQWDMFATPQ YRGVRAGVFLGLGLSGHIPTLHYVISEGFLKAATI GQIGWMLMASLYITGAALYAARIPERFFPGKCD IWFHSHQLFHIFVAGAFVHFHGVSNLQEFRFMI GGGCSEEDAL
3921	A	1587	452	LERDGGCGEEGGSVRSGAGPDSDPGASSPPAG HRGTAASPRPVAAPSRTAPPHTRARASPLPSG PAWRRVQWFSRVSGQVSTLMKATVLMRQPGRV QEIVGALRKGGGDRQLQVISDFDMLSRFAYNGK RCPSSYNILDNSKIISEEKRKELTALLHHYPIEID PHRTVKEKLPHMVEWWTKAHNLLCQKIQKFQI AQVVRESNAMLREGYKTFNTLYHNNIPLFIFSA GIGDILEEIRQMKVFHPNIHIVSNYMDFNEDGFL QGFKGQLIHTYNKNSSACENCGYFQGLEGKTNV ILLGDSIGDLTMADGVPGVQNLKIGFLNDKVEE RRERYMDSYDIVLEKDETLDVVNGLLQHILCQG VQLEMQGP
3922	A	2	164	GKIYQRAFGGHSKLFKGKVQAHGCCCCVADRTG HSILHTSYGRERPAPVHLRQDT
3923	A	2	3258	EHATHAYAKLGTRRRHREVTVFVPTWQLKKNR RVRESHFLTKLHSLKMLSITPSQLENGKKITTYD YRFMVKLAETDGIIVTNEQIHILMNSSKMLMVK DRLLPFTFAGNLFMVPDDPLGRDGPTLDEFLLKP NRLDLDIGNFLKVKWTLPPSSASVTELSDADSG PLESLPNMEEVREEKEERQDEEQRQGQGTQKAA EEDDLDSLASVFRVECPSLSEEILRCLSLHDPDP GALDIDLLPGAASPYLGIPWDGKAPCQQVLAHL AQLTIPSNFTALSFFMGFMDSHRDAIPDYEALVG PLHSLKQKPDWQWDQEHAAFLALKRALVSAL CLMAPNSQLPFRLEVTVSHVALTALHQAHSGRK HPIAYTSKPLLPDEESQGPQSGGDSFYAVA WALK HFSRCIGDTPVVLDLSYASRTTADPEVREGRRVS KAWLIRWSLLVQDKGKRALELALLQGLLGENRL LTPAASMPRFFQVLPFFSDLSTFVCIHMSGYCFYR

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EDEWCAGFGLYVLSPSPVLSFSFSCSPYTPTYA HLAAVACGLERFGQSPLPVVFLTHCNWIFSLWE LLPLWRARGFLSSDGAPLPHPSLLSYIISLTSGLSS LPFIYRTSYRGSFLFAVTVDTLAKQGAQGGGQWW SLPKDVPAPTVPSPHAMGKRPNNLLALQLSDSTLAD IARLQAGQKLSGSSPFSSAFNSLSLDKESGLLMF KGDKKPRVWVVPVQLRRDLIFSVHDIPLGAHQ PEETYKKLRLLGWVPGMQEHVKDYCRSCLFCIP RNLIGSELKVIESPWPLRSTAPWSNLQIEVVG PVTISEEGHKHVLIVADPNTRWVEAFPLKPYHTA VAQVLLQHVFAWGVVPRLEAAQGPQFARHVLVS CGLALGAQVASLSRDLQFPCLTSSGAYWEFKRA LKEFIFLHGKKWAASLPLHLAFRASSTDA TPFKVLTGGESRLTEPLWVEMSSANIEGLKMDV FLLQLVGELLELHWRVADKASEKAENRRFKRES QEKEWNVGDQVLLLSLPRNGSSAKWVGPFYIGD RSLSLYRIWGFPTPEKLGCIYPSSLMKAFAKSG TPLSKVLEQ
3924	A	1	1826	MGSVTVRYFCYGCCLFTSATWTVLLFVYFNSEV TQPLKNVPVKSGSPHGPSKKFYPRFTRGSPSRV LPQFKANKIDDVIDSRVEDPEEGHLKFSSGLMIF NERDQELRDLGYQKHAFNMLISDRLGYHRDVPD TRNAACKEKFYPPDLPAASVVICFYNEAFSALLR TVHSVIDRTPAHLLEHLLVDDSDFDLKGELDE YVQKYLPGKIKVIRNTKREGLIRGRMIGAAHATG EVLVFLDSHCEVNVMWLQPLLAIREDRHTVGC PVIDIISADTLAYSSSPVVRGGFNWGLHFKWDLV PLSELGRAEGATAPIKSPTMAGGLFAMNRQYFH ELGQYDSGMDIWGGENLEISFRIWMCGGKLFIP CSRVGHIKRRPYGSPEGQDTMTHNSRLAHV WLDEYKEQYFSLRDLKTKSYGNISERVELRKKL GCKSFKWYLDNVYPEMQISGSHAKPQQPIFVNR GPKRPKVLQRGLYHLQTNKCLVAQGRPSQKG GLVVLKACDYSDPNQIWIYNEEHVLSLLCLD MSETRSSDPPRLMKCHGSGGSQQWTFGKNNRLY QVSVGQCLRAVDPLGQKGSVAMAICDSSSQ WHLEG
3925	A	5386	2897	VRWNSKTECYLSIQTQENFPANLNLVNCIVISSL VTTQRKLKAMSLGSRNQLARAVLNPMPDFCT KDLLTTTSERIAYLRDFNEDQKKAJETAYAMVK HSPSVAKICLIHGPPGTGKSKTIVGLLYRLLTENQ RKGHSDENSNAKIKQNRVLVCAPSNAAVDELM KKIILEFKEKCKDKKNPLGNCGDINLVRGPEKSI NSEVLKFSLDSQVNHMRMKELPSHVQAMHKKR EFLDYQLDELSRQALCRGGREIQRQELDENISK VSKERQELASKIKEVQGRPQKTQSIHLESHIICCT LSTSGLLLESFAFRGQGGVPFSCVIVDEAGQSCEI ETLTPLIHRCNKLLVGDPKQLPPTVISMKAQEY GYDQSMMARFCRLLEENVEHNMISRLPILQLTVQ YRMHPDICLFPNYYVNRNLKTNRQTEAIRCSSD WPFQPYLVFDVGDGERDNDSDYNVQEIKLVM EIIKLIKDKRKDVFRNIGIITHYKAQKTMIQKDL DKEFDRKGPAEVDTVDAFQGRQKDCVIVTCVRA NSIQGSIGFLASLQRLNVTITRAKYSFILGHLRTL MENQHWNLQIQDAQKRGAIKTCDKNYRHDAV

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				KILKLPVLQRLTHPPTIAPEGSRPQGGPSSKL DSGFAKTSVAASLYHTPSDSKEITLTVTSKDPERP PVHDQLQDPRLLKRMGIEVKGGIFLWDPQPSSPQ HPGATPPTGEPGFVVHQDLSHVQQPAAVVAAL SSHKPPVRGEPPAASPEASTCQSKCDDPEEELCH RREARAFSEGEQEKCGSETHHTRNSRWKRTL EQEDSSSKKRKLL
3926	A	99	284	MPREDRATWKSNYFLKIIQLDDYPKRFIVGANN VGSKQMQQIRMSLRGKAVVLMGKNTMMR
3927	A	542	2	AHLLMLNLAL\TDLL\YLTSLPFLIHYASGENWI FGDFMCKFIRFSHFNL\YSSILFLTCSIFRYCVIIH PMSCFSIHKTRCAVVACAVVWII\SLVAVIPMTFLI TSTNRTNRSACLDLTSSDELNTIKWYNLILTALL CLPLVIVTLCYTTIIHTLTHGHANDSCLKQKARR LTILL
3928	A	1	1516	GEEAVGGGAEGGGFGVGAQGRAGGRGVEAGR MRLSKTLVMDMDADYSAALDPAYTTLEFENVQ VLTMGNDTSPSEGTNLNAPNSLGVSAICAIGDR ATGKHYGASSCDGCKGFFRRSVRKNHMYSCRFS RQCVVDKDKRNQCRYCRLKKCFRAGMKKEAV QNERDRISTRSSYEDSSLPSINALLQAEVLSRQIT SPVSGINGDIRAKKIASIADVCEMKEQLLVLE WAKYIPGFCELPDDQGALLRAHAGEHLLLGAT KRSMVFKDVLLLGNDYIVPRHCELAEMSRVSIR ILDELVLFPQELQIDDNEYAYLKAIIFDPDAKGL SDPGKIKRLRSQVQVSLEDYINDRQYDSRGRFGE LLLLPTLQSITWQMIEQIQFIKLFMAKIDNLLQ EMLLGGSPSDAPHAHHPLHPLMQEHMGNTNVIV ANTMPTHLSNGQMCEWPRPRGQAATPETPQSP PGASGSEPYKLLPGAVATIVKPLSAIPQPTITKQE VI
3929	A	1	2782	RVLSLESLEKDPRLVGAQSVPRGRALKGLSPLG LDSAFRLFPDPRAGPWNTAVLSSGMEPETALWG PDLQGPQSPNDAHRAESENEEESPRQESSGEEI IMGDPAQSPESKDSSTEMSLERSSQDPSVPQNPTP LGHSNPLDHQIPLDPPAPEVVPTPSDWTACEAS WQWGALTTWNSPPVVPANEPSLREL VQGRPAG AEKPYICNECGKSFSQWSKLLRHQRIHTGERPNT CSECGKSFTQSSHLVQHQRTHTGEPYKCPDCG KCFSSWSSNLVQHQRTHTGEPYKCTECEKAFTQ STNLKHQRSHTGEPYKCGECRAFYRSSDLIQ HQATHTGEPYKCECGKRFQGNHNLKHQKIH AGEKPYRCTECGKSFIQSSSELTHQRTHTGEPY ECLECGKSFGHSSTLIKHQRTHLREDPFKCPVCG KTFTLSATLLRHQRTHTGEPYKCECGKSFSVS SNLINHQRIHRGERPYICADCGKSFIMSSTLIRHQ RIHTGEPYKCSDCGKSFISSHLIQHRRTHTGEPY PYKCECGKSFSQSSNLITHVRTHMDENLFCSD CGKAFLEAHELEQHRVIHERGKTPARRAQGDSL LGLGDPSLLTPPPGAKPHKCLVCGKGFNDEGIFM QHQRHIGENPYKNADGLIAHAAPKPPQLRSPRL PFRGNSYPGAAEGRAEAPGQPLKPEQGEGFSQR RGLLSSKTYICSHCGESFLDRSVLLQHQLTHGNE KPFLFPDYRIGLGEAGSPFLSGKPFKCECKQS FGLSSELLHQQVHAGGKSSHKSPELGKSSSVLL

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				EHLRSPLGARPYRCSDCRASFLDRVALTRHQETH TQEKPPNPEDPPPEAVTLSTDQEGEGETPTPTSS SHGEGQNPCTLVEEKPYLCPECGAGFTEVAALLL HRSCHPGVSL
3930	A	513	273	KTQETHIYISEHIFPFLQGFGLNPICMAKTDLSLS HQPDKKGVPSDFILPISDVASIGAGFIYPLVGTG SRESPLWL
3931	A	16	305	KRRDFLSCWPAFTVLGEARGDQVDWSKLYRDT GLVKMSRKPRASSPFSNNHPSTPKRRGRGKHPLI PGPEALSKFPRQPIREKGPVKEVPGTKGSP
3932	A	16	305	KRRDFLSCWPAFTVLGEARGDQVDWSKLYRDT GLVKMSRKPRASSPFSNNHPSTPKRRGRGKHPLI PGPEALSKFPRQPIREKGPVKEVPGTKGSP
3933	A	1	1546	STHASEHWDSALQLAKHLAPDQIPFISKEYAIQLE FAGDYVNALAHYEKGITGDNKEHDEACLAGVA QMSIRMGDIRRGVNQALKHPSRVLKRDCGAILE NMKQFSEAAQLYEKGLYYDKAASVYIRSKNWA KVGDLLPHVSSPKIHLQYAKAKEADGRYKEAVV AYENAKQWQSVIRIYLDHLNNPEKAVNIVRETQ SLDGAKMVARFFLQLDYGSALQFLVMSKCNNE AFTLAQQHNKMEIYADIIGSEDTTNEDYQSIALY FEGEKRYLQAGKFFLLCGQYSRALKHFLKCPSSSE DNVAIEMAETVGQAKDELLTNQLIDHLLGEND GMPKDAKYLFRLYMALKQYREAAQTAIHAREE QSAGNYRNAHDVLFMSYAEKSKQKIPSEMAT NLMILHSYILVKIHVKNGDHMKGARMLIRVANN ISKFPSSHIVPILTSTVIECHRAGLKNSAFSFAAML MRPEYRSKIDAKYKKKIEGMVRRPDISEIEEATTP CPFCKFLLPESELL
3934	A	334	1268	PTRRPILPLTSPKAISVPSPLQGKQHTLVKSCLSVS GIGGFLVSLSSRMKLQTLAVSVTALKFWSAYVP CQTQDRDALRLTLEQIDLIRRMCA SYSELELVT AKALNDTQKLACLIGVEGGHSLDNSLSILRTFYM LGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL TDFGEKVVAEMNRLGMMVDLSHVSDAVARRAL EVSQAPVIFSHSAARGVCNSARNVPDDILQLEE ERWAFVMVSLFHGELIQWQPIRPMCSTVADHFD HIKAVIGSKFIGGDDYDGAGKYRKKTTCKAPW RTSSRMSS
3935	A	1	883	HETTPAVVQSVLLERGWNKFDKQEQAEDWNL YWRSSFRMTEHNSVKPWQQLNHHPGTTKLTR KDCLAKHLKHMRRMYGTSLYQFIPLTFVMPNDY TKFVAEYFQERQMLGTKHSYWICKPAELSRGRG ILIFSDFKDFIDDMYIVQKYISNPLIGRYKCDLR IYVCVTGFKPLTIYVYQEGLVRFATEKFDLSNLQ NNYHLTNSSINKSGASYEKIKEVIGHGCKWTL RFFSYLRSWDVDDLLWKKIHRMVILTILAIAPS VPFAANCFELFGFDILIDDNEFHRTG
3936	A	203	441	HLAHSGLPKHYQYCVRYLYYQVTKDVIKEFA DDGVKYLELRSTPRRENATGMTKKTYVESILEGI KQSKQENLDIDV

TABLE 7

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
1	19	0.930	0.680
2	24	0.964	0.863
3	21	0.990	0.901
4	19	0.981	0.942
5	22	0.991	0.928
6	21	0.956	0.843
8	22	0.913	0.718
9	17	0.997	0.969
11	19	0.930	0.680
13	36	0.983	0.863
14	28	0.935	0.839
15	21	0.997	0.955
16	16	0.983	0.944
17	18	0.989	0.884
19	49	0.996	0.719
20	28	0.972	0.920
21	23	0.954	0.905
22	46	0.955	0.568
23	26	0.942	0.654
24	19	0.979	0.941
25	34	0.884	0.565
26	33	0.934	0.584
27	17	0.975	0.914
28	18	0.980	0.934
29	23	0.928	0.718
30	26	0.978	0.885
32	20	0.946	0.719
33	29	0.933	0.671
35	25	0.996	0.920
36	26	0.903	0.579
40	19	0.981	0.942
47	25	0.971	0.909
53	22	0.991	0.928
55	24	0.960	0.808
60	19	0.986	0.967
78	22	0.913	0.718
86	20	0.883	0.555
87	24	0.982	0.889
88	17	0.997	0.969
115	19	0.930	0.680
134	36	0.983	0.863
136	17	0.913	0.696
137	19	0.958	0.905
140	28	0.935	0.839
143	32	0.914	0.740
153	21	0.997	0.955
154	25	0.913	0.583
155	29	0.972	0.857
169	30	0.977	0.817
170	30	0.977	0.819
171	30	0.977	0.819
175	47	0.926	0.606
176	30	0.968	0.872
177	22	0.957	0.791
192	43	0.930	0.678

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
195	19	0.956	0.860
202	21	0.982	0.871
203	24	0.957	0.870
207	23	0.954	0.905
224	46	0.955	0.568
225	26	0.942	0.654
228	45	0.961	0.839
231	28	0.994	0.937
232	28	0.993	0.896
234	19	0.979	0.942
235	19	0.979	0.941
238	20	0.987	0.943
244	23	0.929	0.683
250	34	0.884	0.565
256	33	0.934	0.584
258	25	0.934	0.729
259	22	0.969	0.871
264	19	0.952	0.753
265	17	0.975	0.914
266	17	0.975	0.914
271	23	0.974	0.884
274	13	0.971	0.834
275	18	0.980	0.934
278	32	0.958	0.668
280	24	0.966	0.881
281	24	0.966	0.881
286	23	0.928	0.718
291	35	0.991	0.824
293	27	0.956	0.806
294	23	0.952	0.827
301	26	0.978	0.885
316	20	0.946	0.719
320	28	0.978	0.726
327	29	0.933	0.671
331	48	0.903	0.571
345	25	0.996	0.920
349	26	0.903	0.579
351	24	0.951	0.876
352	18	0.944	0.716
353	32	0.992	0.854
354	27	0.945	0.817
355	16	0.922	0.716
356	13	0.959	0.818
357	23	0.986	0.878
358	19	0.904	0.671
359	16	0.988	0.951
360	15	0.981	0.938
361	18	0.944	0.716
362	21	0.984	0.869
363	40	0.979	0.813
364	18	0.883	0.693
365	22	0.962	0.908
366	22	0.961	0.827
367	44	0.941	0.624
368	20	0.952	0.791
369	22	0.949	0.840
370	28	0.957	0.682

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
372	28	0.974	0.894
373	19	0.972	0.947
374	29	0.968	0.785
375	19	0.949	0.897
377	23	0.962	0.910
378	31	0.974	0.895
379	26	0.969	0.939
380	27	0.945	0.817
383	27	0.945	0.817
384	25	0.992	0.877
385	32	0.983	0.825
386	44	0.924	0.564
387	26	0.971	0.894
388	19	0.989	0.862
389	24	0.990	0.947
390	34	0.942	0.635
391	16	0.922	0.716
394	19	0.987	0.970
398	36	0.992	0.866
404	13	0.959	0.818
417	23	0.986	0.878
421	19	0.904	0.671
425	28	0.971	0.717
431	16	0.988	0.951
452	18	0.944	0.716
459	21	0.991	0.902
468	21	0.984	0.869
478	40	0.979	0.813
486	18	0.883	0.693
499	22	0.962	0.908
501	19	0.962	0.877
514	44	0.941	0.624
529	20	0.952	0.791
533	39	0.914	0.719
548	28	0.957	0.682
561	28	0.974	0.894
562	28	0.974	0.893
564	18	0.949	0.806
576	19	0.972	0.947
584	29	0.968	0.785
585	28	0.973	0.810
591	19	0.949	0.897
592	24	0.991	0.954
594	20	0.985	0.959
595	20	0.985	0.959
612	23	0.962	0.910
619	31	0.974	0.895
621	15	0.959	0.795
633	26	0.969	0.939
640	20	0.949	0.842
645	25	0.911	0.759
684	25	0.992	0.877
691	32	0.983	0.825
698	44	0.924	0.564
700	19	0.982	0.941
710	26	0.971	0.894
714	23	0.965	0.907

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (MAXIMUM SCORE)	MeanS (Mean Score)
718	19	0.989	0.862
725	21	0.976	0.851
728	33	0.961	0.895
734	25	0.963	0.660
741	34	0.942	0.635
744	19	0.959	0.924
747	16	0.922	0.716
756	26	0.973	0.864
767	22	0.986	0.943
768	27	0.916	0.758
769	19	0.987	0.970
770	22	0.981	0.933
771	34	0.993	0.893
773	20	0.968	0.939
774	21	0.971	0.945
778	22	0.986	0.943
779	32	0.973	0.846
781	23	0.950	0.857
785	27	0.916	0.758
786	27	0.916	0.758
788	22	0.981	0.933
793	22	0.986	0.803
794	39	0.892	0.654
797	27	0.965	0.847
810	22	0.981	0.933
823	34	0.993	0.893
825	17	0.962	0.778
837	20	0.968	0.939
844	25	0.984	0.951
845	17	0.919	0.706
846	21	0.971	0.945
847	21	0.971	0.945
890	22	0.986	0.943
893	24	0.971	0.865
894	24	0.971	0.865
896	32	0.973	0.846
899	31	0.982	0.817
922	15	0.882	0.706
924	21	0.975	0.948
925	21	0.927	0.661
933	20	0.967	0.906
960	20	0.967	0.906
967	38	0.970	0.784
968	47	0.970	0.557
972	36	0.945	0.775

TABLE 8

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3955	A	235	1272	GPREVLAASSLADGSEEQVMAVALVRERDLSFPG VGDAVVNPTRWHLPAQPEMLYEGGEGRMETLK

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				DKTLQELEELQNDSE AIDQLALESPEVQDLQLERE MALATNRS LAERNLEFQGP LEISRSNLS DRYQELR KLVERCQE QKAKLEKFSSALQP GTLLDLLQVEGM KIEESEAMA EKFLGEVPLETFLENFSSMRMLSH LRRVRVEKLQEVVRKPRASQELAGDAPPPRSPPP VPPSPPGNTPCG*RAAAATISHASLPFALQIPQPA CGPHCPWSPATGPPFPSSVPALLLQRASGPHLPGSP AWTQGCGCLLLVPTEEHAAPPYGFPPPPGPAWPG Y
3956	A	821	385	SICADRTERVGIFFYIPAGTTDEADVTHP*EGHSYL SNHAGIQRSSRP/SHYQGE/WHDNCF TADELQLLT YQLCHTYVRCTRSVSIPAPAYY AHLVAFRARYHL VDKEHDSAEGSHVSGQSNGRDPQALAKAVQIHQ DTLRTMYFA
3957	A	4621	240	ELISTFKLLLEKKRSEVMKMKKRYEVGLEKLD SA SSQVATMQMELEALHPQLKVASKEVDEMIMIE KESVEVAKTEKIVKADETIANEQAMASKAIKDEC DADLAGALPIESALAA DTLTAQDITVVKSMKSP PAGVKLVME AICILKGIKADKIPDPTGSGKKIEDF WGP AKRLLGDMRFLQSLHEYDKDNIPPA YMNIIR KNYIPNPDFVPEKIRNASTAAEGLCKWVIAMDSY DKVAKIVAPKKIKLAAE GELKIAMDGLRKKQA ALKEVQDKLARLQDTLELNKQKKADLENQVDLC SKKLERAELIGGLGGEKTRWSHTALELGQLYIN LTGDILISSGVVAYLGAF TSTYRQNQTKEWTTLCK GRDIPCSDDCSLMGTLGEAVTIRTWN IAGLP SDFS SIDNGIIIMNARRWPL MIDPQSQANKWIKNMEKA NSLYVIKLSEPDYVRTLENCIQFGTPV LLENVGEE LDPILEPLLLKQTFKQGGSTCIRLGDSTIEYAPDFR FYITTKLRNPHYLPETSVKVTLLNFMITPEGMQDQ LLGIVVAQERPDLEEEKQALILQGAENKRQLKEIE DKILEVLSSEGNILEDETAIKILSSSKALANEISQK QEVAEETEKKIDTRMGYRPIAHSSILFFSLADLA NIEPMYQYSLTWFINLFILSIENSEKSEILAKRLQIL KDHF TYSLYVNVCRSLFEKDKLLFSFCLTINLLH ERAINKA EWRFLLTGGIGLDN PYANPCTWLPQKS WDEICRLDDLPAFKTIRREFMRLKDGWKKVYDSL EPHHEVFPEEWEDKANEFQRM LIIRCLRPDKVIPM LQEFIINRLGRAFI EPPFDLAKAFGDSNCCAPLIFV LSPGADPMAALLKFADDQGYGGSKLSSLGQGGQ GPIAMKMLEKAVKEGTWVVLQNCHLATSWMPT LEKVCEELSPETHPD FRMWLTSYSPNFPVSVLQ NGVKMTNEAPKGLRANIIRSYLMDPISDPEFFGSC KKPEEFKLLYGLCFFHALVQERRKFGPLWWNIP YEFNETDLRISVQQLHMF LNQYEELPYEALRYMT GECNYGGRVTDDWDRRTLRSILNKFFNP ELVENS DYKFDSSGIYFVPPSGDHKSYIEYTKLPLTPAPEI FGMNANADITKDQSETQLLFDNILLTQSR SAGAG AKSSDEVVNEVASDILGKLPNNFDIEAAMRRYPT TYTQSMNTVLVQEMGRFNKLLKTIRDSCVN IQKA IKGLAVMSTDLEEVVSSILNVKIPEMWMGKSYP LKPLGSYVNDFLARLKFLQQWYEVGPPPVFWSG FFFTQAFLTGAQQNYARKY TIPIDLLGFDYEV MED KEYKHPPEDGVFIHGLFDGASWNRKIKKLAESH PKILYDTPVMWLKPCKRADIPKRPSYVAPLYKT

SEQ ID NO:	Method	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
				SERRGVLSTTGHSTNFVIAIMTLPSDQPKHEHWIGR GVALLCQLNS
3958	A	35	529	GADMAKSKNHTTHNQSRKWHNRVIKKPLSQRYSK SLKGVDPKFLGNMCFKKKKKKGLKKMQADSA KAVSTCAKAIEALVKPKEVKPKIPKGVSCEN*LA YIAYPKFWTCACACIAKGLRLCQPKAKAQDQTK AQVQIKAQAAAPASVPTQAPKGAQAPTKASG
3959	A	1883	763	LLVLLRLTNLLIASSTRISRATLTCSPPGIPVDPRVR PRVRSHLVMYLGITTGSLHKA VVSGDSSAHLVEEI QLFPDPEPVRNLQLAPTQGA VFGSGGVWRVPR ANCSVYESCVDCVLARDPHCA WDPESRTCCLLSA PNLNSWKQDMERGNPEWACASGPMRSRLRPQSR PQIIEVLAVPNSILELPCPHLSALASYWSHGPAA VPEASSTVYNGSLLLIVQDGVGGLYQCWATENG SYPVISYWVDSQDQTLALDPELAGIPREHVKVPLT RVSGGAALAAQQSYWPHFVTVTVLFAVLVSGALI ILVASPLRALRARGKVQGCETLRPGEKAPLSREQH LQSPKECRTSASDVEDADNCLGTEVA
3960	A	1	481	SYAAPSLFVKSLYWALAFMAVLLAVSGVVIVVLA SRAGARCQCQPPGWVLSEEHCYFSAEAQAWEA SQAFCSAYHATLPLLSHTQDFLGRYPVSRHSWVG AWRGPGQWHWIDEAPLPQLPEDGEDNLDINCG ALEEGLVAANCSTPRPWVCAKGTQ

TABLE 9

SEQ ID NO:	Accession Number	Species	Description	Smith Waterman Score	% Identity
3937	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	193	25
3938	AF093097	Homo sapiens	putative RNA-binding protein Q99	3881	84
3939	AB012308	Anthocidaris crassispina	B2HC	4169	74
3940	U10248	Homo sapiens	ribosomal protein L29	787	95
3941	Y99418	Homo sapiens	Human PRO1317 (UNQ783) amino acid sequence SEQ ID NO:277.	4031	100
3942	AL023516	Gallus gallus	B locus C type Lectin	198	35

5

TABLE 10

SEQ ID NO:	Accession No.	Description	Results*
3937	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.168e-11 209-224
3942	BL00615	C-type lectin domain proteins.	BL00615A 16.68 6.400e-11 37-55

* Results Include in order: accession number subtype; raw score; p-value; position of signature in amino acid sequence

TABLE 11

SEQ ID NO:	PFAM Name	Description	P-Value	PFAM Score
3938	Piwi	Piwi domain	2.6e-150	512.7
3940	Ribosomal_L29e	Ribosomal L29e protein family	2.3e-19	77.8
3941	Sema	Sema domain	4e-181	615.1
3942	lectin_c	Lectin C-type domain	0.086	-7.1

5

TABLE 12

SEQ ID NO:	Position of end of Signal in Amino Acid Sequence	MaxS (Maximum Score)	Means (Mean Score)
3941	31	0.985	0.926
3942	21	0.974	0.894

TABLE 13

10

SEQ ID NO: of full length nucleotide sequence	SEQ ID NO: of full length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Priority Docket number corresponding SEQ ID NO: in priority application	SEQ ID NO: in USSN 09/496,914
3937	3943	3949	3955	787CIP2G_1	787_3587
3938	3944	3950	3956	787CIP2G_2	787_3813
3939	3945	3951	3957	787CIP2G_3	787_4462
3940	3946	3952	3958	787CIP2G_4	787_4887
3941	3947	3953	3959	787CIP2G_5	787_5794
3942	3948	3954	3960	787CIP2G_6	787_8743

TABLE 14

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
adult brain	GIBCO	ABD003	3940
adult brain	Clontech	ABR006	3940
adult brain	Invitrogen	ABR014	3940
cultured preadipocytes	Stratagene	ADP001	3937
adult heart	GIBCO	AHR001	3940
adult kidney	GIBCO	AKD001	3940
adult lung	GIBCO	ALG001	3940
young liver	GIBCO	ALV001	3940
adult ovary	Invitrogen	AOV001	3938, 3940-3941
adult spleen	GIBCO	ASP001	3940-3941
testis	GIBCO	ATS001	3940
bone marrow	Clontech	BMD001	3938, 3940
bone marrow	Clontech	BMD004	3940
adult cervix	BioChain	CVX001	3940
endothelial cells	Stratagene	EDT001	3940
fetal brain	Clontech	FBR006	3940
fetal brain	Invitrogen	FBT002	3940-3941
fetal heart	Invitrogen	FHR001	3940
fetal kidney	Clontech	FKD001	3940
fetal kidney	Clontech	FKD002	3940

TISSUE ORIGIN	LIBRARY/ RNA SOURCE	HYSEQ LIBRARY NAME	SEQ ID NOS:
fetal liver-spleen	Columbia University	FLS001	3937, 3940
fetal liver-spleen	Columbia University	FLS002	3938, 3941
fetal liver-spleen	Columbia University	FLS003	3940
fetal liver	Clontech	FLV004	3940
fetal skin	Invitrogen	FSK001	3940-3942
fetal spleen	BioChain	FSP001	3940
fetal brain	GIBCO	HFB001	3937, 3940-3941
infant brain	Columbia University	IB2002	3937, 3939, 3941
leukocyte	GIBCO	LUC001	3940-3941
leukocyte	Clontech	LUC003	3940-3941
melanoma from cell line ATCC #CRL 1424	Clontech	MEL004	3940
mammary gland	Invitrogen	MMG001	3937, 3940-3941
neuronal cells	Stratagene	NTU001	3937, 3942
prostate	Clontech	PRT001	3938
rectum	Invitrogen	REC001	3940
salivary gland	Clontech	SALs03	3941
small intestine	Clontech	SIN001	3940
skeletal muscle	Clontech	SKM001	3940
spinal cord	Clontech	SPC001	3940
thymus	Clontech	THMc02	3938
thyroid gland	Clontech	THR001	3942
uterus	Clontech	UTR001	3940

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-984, 1969-2952, 3937-3942 or 3949-3954, a full length protein coding portion of SEQ ID NO:1-984, 1969-2952, 3937-3942 or 3949-3954, a mature protein coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, an active domain coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, and complementary sequences thereof.
2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
6. A vector comprising the polynucleotide of claim 1.
7. An expression vector comprising the polynucleotide of claim 1.
8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:
 - (a) a polypeptide encoded by any one of the polynucleotides of claim 1; and
 - (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954.

11. A composition comprising the polypeptide of claim 10 and a carrier.
12. An antibody directed against the polypeptide of claim 10.
13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
 - b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
 - a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
 - b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
 - c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
16. A method for detecting the polypeptide of claim 10 in a sample, comprising:
 - a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
 - a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, a mature protein coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, an active domain coding portion of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 985-1968, 2953-3936, 3943-3948 or 3955-3960, the mature protein portion thereof, or the active domain thereof.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1-984, 1969-2952, 3937-3942 or 3949-3954.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

SEQUENCE LISTING

<110> Hyseq, Inc.
Tang, Y. Tom et al

<120> Novel Nucleic Acids and Polypeptides

<130> 21272-029

<140> Not Yet Assigned

<141> 2001-02-05

<150> Not Yet Assigned

<151> 2001-01-30

<150> 09/728,422

<151> 2000-11-30

<150> 09/693,325

<151> 2000-10-20

<150> 09/663,561

<151> 2000-09-15

<150> 09/654,936

<151> 2000-09-01

<150> 09/620,325

<151> 2000-07-19

<150> 09/598,075

<151> 2000-06-20

<150> 09/560,875

<151> 2000-04-27

<150> 09/496,914

<151> 2000-02-03

<160> 3960

<170> Custom

<210> 1

<211> 1867

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (416) .. (814)

<400> 1

taccggtccg gaattcccgg gtcgacccac gcgtccggcc aaggttgcgg gtcattggagt	60
cccgaaccct cctcctgctg ttctcgggag ccgtggccct gatccagacc tgggcagatt	120
acaattacaa tcaaggcaga aatgatctca tttttacatt acaactctgg aaaaggcaat	180
agactgagat gcaagtgtgc cccaagtga tgggcagaag gagagaaggt gttttggatg	240
cattctagaa cacaggtaat ctaaggagag ttgatcaagg ccgtggaaga gtcctccagc	300

2

```

taggtagcct catccctgcc actgtgtttg ctccatttat gtacccatcc taccggcct 1577
gggctgaccc atggggaagg ctggctaatt tcagtgttc tgcttggttg ttcagggcca 1637
tttcaggttt ggggtgtttc tggggatggt aacatgggat tcaggctcaa ctacaagaa 1697
acttttccat ctcatgatgg gatgctgttg ggcattgtcca atgtatgact tcatgagtta 1757
cacagggtgct aattcgtagg ggcacttggg atcacatggg tgttttttgt ccatgggtcaa 1817
gcatttatct tatcagggtc acagtaacat gcaaaagtgc ttccacattt 1867

```

```

<210> 2
<211> 2586
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(2553)

```

```

<400> 2
aaa gca ata agg atg ttt aag tgc tgg tca gtt gtc ttg gtt ctc gga 48
Lys Ala Ile Arg Met Phe Lys Cys Trp Ser Val Val Leu Val Leu Gly
1 5 10 15

ttc att ttt ctg gag tgc gaa gga agg cca acc aaa gaa gga gga tat 96
Phe Ile Phe Leu Glu Ser Glu Gly Arg Pro Thr Lys Glu Gly Gly Tyr
20 25 30

ggc ctt aaa tcc tat cag cct cta atg aga ttg cga cat aag cag gaa 144
Gly Leu Lys Ser Tyr Gln Pro Leu Met Arg Leu Arg His Lys Gln Glu
35 40 45

aaa aat caa gaa agt tca aga gtc aaa gga ttt atg att cag gat ggc 192
Lys Asn Gln Glu Ser Ser Arg Val Lys Gly Phe Met Ile Gln Asp Gly
50 55 60

cct ttg gga tct tgt gaa aat aag tac tgt ggt ttg gga aga cac tgt 240
Pro Leu Gly Ser Cys Glu Asn Lys Tyr Cys Gly Leu Gly Arg His Cys
65 70 75 80

gtt gcc agc aga gag aca ggg caa gca gaa tgt gcc tgt atg gac ctt 288
Val Ala Ser Arg Glu Thr Gly Gln Ala Glu Cys Ala Cys Met Asp Leu
85 90 95

tgc aaa cgt cac tac aga cct gtg tgt gga tct gac gga gaa ttc tat 336
Cys Lys Arg His Tyr Arg Pro Val Cys Gly Ser Asp Gly Glu Phe Tyr
100 105 110

gaa aac cac tgt gaa gtg cac aga gct gct tgc ctg aaa aaa caa aag 384
Glu Asn His Cys Glu Val His Arg Ala Ala Cys Leu Lys Lys Gln Lys
115 120 125

att acc att gtt cac aat gaa gac tgc ttc ttt aaa gga gat aag tgc 432
Ile Thr Ile Val His Asn Glu Asp Cys Phe Phe Lys Gly Asp Lys Cys
130 135 140

aag act act gaa tac agc aag atg aaa aat atg cta tta gat tta caa 480
Lys Thr Thr Glu Tyr Ser Lys Met Lys Asn Met Leu Leu Asp Leu Gln

```

145	150	155	160	
aat caa aaa tat att atg caa gaa aat gaa aat cct aat ggc gac gac				528
Asn Gln Lys Tyr Ile Met Gln Glu Asn Glu Asn Pro Asn Gly Asp Asp	165	170	175	
ata tct cgg aag aag cta ttg gtg gat caa atg ttt aaa tat ttt gat				576
Ile Ser Arg Lys Lys Leu Leu Val Asp Gln Met Phe Lys Tyr Phe Asp	180	185	190	
gca gac agt aat gga ctt gta gat att aat gaa cta act cag gtg ata				624
Ala Asp Ser Asn Gly Leu Val Asp Ile Asn Glu Leu Thr Gln Val Ile	195	200	205	
aaa cag gaa gaa ctt ggc aag gat ctc ttt gat tgt act ttg tat gtt				672
Lys Gln Glu Glu Leu Gly Lys Asp Leu Phe Asp Cys Thr Leu Tyr Val	210	215	220	
cta ttg aaa tat gat gat ttt aat gct gac aag cac ctg gct ctt gaa				720
Leu Leu Lys Tyr Asp Asp Phe Asn Ala Asp Lys His Leu Ala Leu Glu	225	230	235	240
gaa ttt tat aga gca ttc caa gtg atc cag ttg agt ctg cca gaa gat				768
Glu Phe Tyr Arg Ala Phe Gln Val Ile Gln Leu Ser Leu Pro Glu Asp	245	250	255	
cag aaa cta agc atc act gca gca act gtg gga caa agt gct gtt ctg				816
Gln Lys Leu Ser Ile Thr Ala Ala Thr Val Gly Gln Ser Ala Val Leu	260	265	270	
agc tgt gcc att caa gga acc ctg aga cct ccc att atc tgg aaa agg				864
Ser Cys Ala Ile Gln Gly Thr Leu Arg Pro Pro Ile Ile Trp Lys Arg	275	280	285	
aac aat att att cta aat aat tta gat ttg gaa gac atc aat gac ttt				912
Asn Asn Ile Ile Leu Asn Asn Leu Asp Leu Glu Asp Ile Asn Asp Phe	290	295	300	
gga gat gat ggg tcc ttg tat att act aag gtt acc aca act cac gtt				960
Gly Asp Asp Gly Ser Leu Tyr Ile Thr Lys Val Thr Thr Thr His Val	305	310	315	320
ggc aat tac acc tgc tat gca gat ggc tat gaa caa gtc tat cag act				1008
Gly Asn Tyr Thr Cys Tyr Ala Asp Gly Tyr Glu Gln Val Tyr Gln Thr	325	330	335	
cac atc ttc caa gtg aat gtt cct cca gtc atc cgg gtg tat cca gag				1056
His Ile Phe Gln Val Asn Val Pro Pro Val Ile Arg Val Tyr Pro Glu	340	345	350	
agt cag gct aga gag cct ggg gta act gcc agt ctt agg tgc cat gca				1104
Ser Gln Ala Arg Glu Pro Gly Val Thr Ala Ser Leu Arg Cys His Ala	355	360	365	
gag ggc ata cca aag cct cag ctt ggc tgg ttg aag aat gga att gat				1152
Glu Gly Ile Pro Lys Pro Gln Leu Gly Trp Leu Lys Asn Gly Ile Asp	370	375	380	
att aca cca aag ctt tcc aaa caa ctc acg ctt caa gca aat ggc agt				1200
Ile Thr Pro Lys Leu Ser Lys Gln Leu Thr Leu Gln Ala Asn Gly Ser	385	390	395	400
gag gtt cac ata agc aat gtg cgc tat gaa gat act gga gca tac act				1248
Glu Val His Ile Ser Asn Val Arg Tyr Glu Asp Thr Gly Ala Tyr Thr				

405	410	415	
tgt atc gca aag aat gaa gca gga gtg tat gaa gac atc tct tct ctt Cys Ile Ala Lys Asn Glu Ala Gly Val Tyr Glu Asp Ile Ser Ser Leu 420 425 430			1296
ttt gtg gaa gac tct gct aga aag acc cta gct aac ata tta tgg aga Phe Val Glu Asp Ser Ala Arg Lys Thr Leu Ala Asn Ile Leu Trp Arg 435 440 445			1344
gaa gaa ggt ctg gga att ggg aac atg ttc tat gtt ttt tat gaa gat Glu Glu Gly Leu Gly Ile Gly Asn Met Phe Tyr Val Phe Tyr Glu Asp 450 455 460			1392
gga atc aaa gtg ata caa ccc ata gaa tgt gaa ttt cag agg cac att Gly Ile Lys Val Ile Gln Pro Ile Glu Cys Glu Phe Gln Arg His Ile 465 470 475 480			1440
aag cct agt gaa aag ctc ctt gga ttt cag gat gaa gtc tgt ccc aaa Lys Pro Ser Glu Lys Leu Leu Gly Phe Gln Asp Glu Val Cys Pro Lys 485 490 495			1488
gct gag gga gat gaa gtt cag agg tgt gtg tgg gca tca gct gtt aat Ala Glu Gly Asp Glu Val Gln Arg Cys Val Trp Ala Ser Ala Val Asn 500 505 510			1536
gtc aaa gac aag ttc att tat gtt gca cag cca act ttg gac aga gtc Val Lys Asp Lys Phe Ile Tyr Val Ala Gln Pro Thr Leu Asp Arg Val 515 520 525			1584
ctt att gtt gat gtg cag tcc caa aaa gtt gtt cag gca gtg agc aca Leu Ile Val Asp Val Gln Ser Gln Lys Val Val Gln Ala Val Ser Thr 530 535 540			1632
gac cct gtc cca gtt aaa tta cac tat gac aaa tca cat gat cag gtc Asp Pro Val Pro Val Lys Leu His Tyr Asp Lys Ser His Asp Gln Val 545 550 555 560			1680
tgg gtg cta agc tgg ggt acc ttg gag aag aca tca cca aca cta cag Trp Val Leu Ser Trp Gly Thr Leu Glu Lys Thr Ser Pro Thr Leu Gln 565 570 575			1728
gta att acc ctg gcc agt ggg aat gtg cct cac cac acg atc cac acc Val Ile Thr Leu Ala Ser Gly Asn Val Pro His His Thr Ile His Thr 580 585 590			1776
caa cca gtg gga aag caa ttt gac aga gtg gat gat ttt ttc att ccc Gln Pro Val Gly Lys Gln Phe Asp Arg Val Asp Asp Phe Phe Ile Pro 595 600 605			1824
acc aca aca ctc att atc acc cat atg agg ttt gga ttt att ctt cat Thr Thr Thr Leu Ile Ile Thr His Met Arg Phe Gly Phe Ile Leu His 610 615 620			1872
aaa gat gaa gct gca cta caa aaa att gat ctt gaa acc atg tca tac Lys Asp Glu Ala Ala Leu Gln Lys Ile Asp Leu Glu Thr Met Ser Tyr 625 630 635 640			1920
atc aag aca att aac ttg aag gac tat aag tgc gtt cct cag tca ttg Ile Lys Thr Ile Asn Leu Lys Asp Tyr Lys Cys Val Pro Gln Ser Leu 645 650 655			1968
gca tat aca cac ttg gga ggc tac tac ttc att ggc tgc aaa cct gac Ala Tyr Thr His Leu Gly Gly Tyr Tyr Phe Ile Gly Cys Lys Pro Asp 660 665 670 675 680 685 690 695 700			2016

660	665	670	
agc acc gga gca gtt tcc cca cag gtc atg gtg gac ggt gta act gac Ser Thr Gly Ala Val Ser Pro Gln Val Met Val Asp Gly Val Thr Asp 675 680 685			2064
tca gtc att ggg ttc aat agt gat gtg acg ggc act cca tat gtc tct Ser Val Ile Gly Phe Asn Ser Asp Val Thr Gly Thr Pro Tyr Val Ser 690 695 700			2112
cca gat ggc cac tac ctt gtc agc att aat gat gtg aaa ggt ctt gta Pro Asp Gly His Tyr Leu Val Ser Ile Asn Asp Val Lys Gly Leu Val 705 710 715 720			2160
agg gtt cag tac att acc atc aga gga gaa ata cag gag gct ttt gat Arg Val Gln Tyr Ile Thr Ile Arg Gly Glu Ile Gln Glu Ala Phe Asp 725 730 735			2208
att tac aca aat ctg cac ata tct gat ctg gca ttt caa cca tcc ttt Ile Tyr Thr Asn Leu His Ile Ser Asp Leu Ala Phe Gln Pro Ser Phe 740 745 750			2256
act gaa gcc cac caa tat aac atc tac ggt agt tca agc aca caa act Thr Glu Ala His Gln Tyr Asn Ile Tyr Gly Ser Ser Ser Thr Gln Thr 755 760 765			2304
gat gtg ctc ttt gtg gag ctc tct tct ggg aag gtc aag atg ata aag Asp Val Leu Phe Val Glu Leu Ser Ser Gly Lys Val Lys Met Ile Lys 770 775 780			2352
agt ctc aag gaa cca ctc aag gca gaa gaa tgg cct tgg aac cgg aaa Ser Leu Lys Glu Pro Leu Lys Ala Glu Glu Trp Pro Trp Asn Arg Lys 785 790 795 800			2400
aac agg caa atc cag gac agt ggc ttg ttt ggt caa tac ctg atg aca Asn Arg Gln Ile Gln Asp Ser Gly Leu Phe Gly Gln Tyr Leu Met Thr 805 810 815			2448
cct tcc aag gac tct ctc ttc atc cta gat gga cga ctc aat aaa tta Pro Ser Lys Asp Ser Leu Phe Ile Leu Asp Gly Arg Leu Asn Lys Leu 820 825 830			2496
aac tgt gag atc act gaa gtt gaa aaa gga aat aca gtc att tgg gtt Asn Cys Glu Ile Thr Glu Val Glu Lys Gly Asn Thr Val Ile Trp Val 835 840 845			2544
gga gat gcc taaaaaccct aggggtacaat tattgaatga agg Gly Asp Ala 850			2586

<210> 3
 <211> 2856
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (182)..(2593)

<400> 3

```

aaattggtat agcagtagcc agctggctag cgtttaaact taagcttggt accgagctcg      60
gatccactag tccagtgtgg tggaattccg cggctggagg tgtgaggatc cgaacccagg      120
ggtaggggggt ggaggcggct cctgcgacgc aaggggactt gagactcacc ggccgcacgc      180
c   atg agg gcc ctg tgg gtg ctg ggc ctc tgc tgc gtc ctg ctg acc      226
    Met Arg Ala Leu Trp Val Leu Gly Leu Cys Cys Val Leu Leu Thr
      1             5             10             15

ttc ggg tgc gtc aga gct gac gat gaa gtt gat gtg gat ggt aca gta      274
Phe Gly Ser Val Arg Ala Asp Asp Glu Val Asp Val Asp Gly Thr Val
      20             25             30

gaa gag gat ctg ggt aaa agt aga gaa gga tca agg acg gat gat gaa      322
Glu Glu Asp Leu Gly Lys Ser Arg Glu Gly Ser Arg Thr Asp Asp Glu
      35             40             45

gta gta cag aga gag gaa gaa gct att cag ttg gat gga tta aat gca      370
Val Val Gln Arg Glu Glu Glu Ala Ile Gln Leu Asp Gly Leu Asn Ala
      50             55             60

tca caa ata aga gaa ctt aga gag aag tgc gaa aag ttt gcc ttc caa      418
Ser Gln Ile Arg Glu Leu Arg Glu Lys Ser Glu Lys Phe Ala Phe Gln
      65             70             75

gcc gaa gtt aac aga atg atg aaa ctt atc atc aat tca ttg tat aaa      466
Ala Glu Val Asn Arg Met Met Lys Leu Ile Ile Asn Ser Leu Tyr Lys
      80             85             90             95

aat aaa gag att ttc ctg aga gaa ctg att tca aat gct tct gat gct      514
Asn Lys Glu Ile Phe Leu Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala
      100            105            110

tta gat aag ata agg cta ata tca ctg act gat gaa aat gct ctt tct      562
Leu Asp Lys Ile Arg Leu Ile Ser Leu Thr Asp Glu Asn Ala Leu Ser
      115            120            125

gga aat gag gaa cta aca gtc aaa att aag tgt gat aag gag aag aac      610
Gly Asn Glu Glu Leu Thr Val Lys Ile Lys Cys Asp Lys Glu Lys Asn
      130            135            140

ctg ctg cat gtc aca gac acc ggt gta gga atg acc aga gaa gag ttg      658
Leu Leu His Val Thr Asp Thr Gly Val Gly Met Thr Arg Glu Glu Leu
      145            150            155

gtt aaa aac ctt ggt acc ata gcc aaa tct ggg aca agc gag ttt tta      706
Val Lys Asn Leu Gly Thr Ile Ala Lys Ser Gly Thr Ser Glu Phe Leu
      160            165            170            175

aac aaa atg act gaa gca cag gaa gat ggc cag tca act tct gaa ttg      754
Asn Lys Met Thr Glu Ala Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu
      180            185            190

att ggc cag ttt ggt gtc ggt ttc tat tcc gcc ttc ctt gta gca gat      802
Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp
      195            200            205

aag gtt att gtc act tca aaa cac aac aac gat acc cag cac atc tgg      850
Lys Val Ile Val Thr Ser Lys His Asn Asn Asp Thr Gln His Ile Trp
      210            215            220

gag tct gac tcc aat gaa ttt tct gta att gct gac cca aga gga aac      898
Glu Ser Asp Ser Asn Glu Phe Ser Val Ile Ala Asp Pro Arg Gly Asn

```

225	230	235	
act cta gga cgg gga acg aca att acc ctt gtc tta aaa gaa gaa gca			946
Thr Leu Gly Arg Gly Thr Thr Ile Thr Leu Val Leu Lys Glu Glu Ala			
240	245	250	255
tct gat tac ctt gaa ttg gat aca att aaa aat ctc gtc aaa aaa tat			994
Ser Asp Tyr Leu Glu Leu Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr			
260	265		270
tca cag ttc ata aac ttt cct att tat gta tgg agc agc aag act gaa			1042
Ser Gln Phe Ile Asn Phe Pro Ile Tyr Val Trp Ser Ser Lys Thr Glu			
275	280		285
act gtt gag gag ccc atg gag gaa gaa gaa gca gcc aaa gaa gag aaa			1090
Thr Val Glu Glu Pro Met Glu Glu Glu Glu Ala Ala Lys Glu Glu Lys			
290	295		300
gaa gaa tct gat gat gaa gct gca gta gag gaa gaa gaa gaa gaa aag			1138
Glu Glu Ser Asp Asp Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys			
305	310		315
aaa cca aag act aaa aaa gtt gaa aaa act gtc tgg gac tgg gaa ctt			1186
Lys Pro Lys Thr Lys Lys Val Glu Lys Thr Val Trp Asp Trp Glu Leu			
320	325		330
atg aat gat atc aaa cca ata tgg cag aga cca tca aaa gaa gta gaa			1234
Met Asn Asp Ile Lys Pro Ile Trp Gln Arg Pro Ser Lys Glu Val Glu			
340	345		350
gaa gat gaa tac aaa gct ttc tac aaa tca ttt tca aag gaa agt gat			1282
Glu Asp Glu Tyr Lys Ala Phe Tyr Lys Ser Phe Ser Lys Glu Ser Asp			
355	360		365
gac ccc atg gct tat att cac ttt act gct gaa ggg gaa gtt acc ttc			1330
Asp Pro Met Ala Tyr Ile His Phe Thr Ala Glu Gly Glu Val Thr Phe			
370	375		380
aaa tca att tta ttt gta ccc aca tct gct cca cgt ggt ctg ttt gac			1378
Lys Ser Ile Leu Phe Val Pro Thr Ser Ala Pro Arg Gly Leu Phe Asp			
385	390		395
gaa tat gga tct aaa aag agc gat tac att aag ctc tat gtg cgc cgt			1426
Glu Tyr Gly Ser Lys Lys Ser Asp Tyr Ile Lys Leu Tyr Val Arg Arg			
400	405		410
gta ttc atc aca gac gac ttc cat gat atg atg cct aaa tac ctc aat			1474
Val Phe Ile Thr Asp Phe His Asp Met Met Pro Lys Tyr Leu Asn			
420	425		430
ttt gtc aag ggt gtg gtg gac tca gat gat ctc ccc ttg aat gtt tcc			1522
Phe Val Lys Gly Val Val Asp Ser Asp Asp Leu Pro Leu Asn Val Ser			
435	440		445
cgc gag act ctt cag caa cat aaa ctg ctt aag gtg att agg aag aag			1570
Arg Glu Thr Leu Gln Gln His Lys Leu Leu Lys Val Ile Arg Lys Lys			
450	455		460
ctt gtt cgt aaa acg ctg gac atg atc aag aag att gct gat gat aaa			1618
Leu Val Arg Lys Thr Leu Asp Met Ile Lys Lys Ile Ala Asp Asp Lys			
465	470		475
tac aat gat act ttt tgg aaa gaa ttt ggt acc aac atc aag ctt ggt			1666
Tyr Asn Asp Thr Phe Trp Lys Glu Phe Gly Thr Asn Ile Lys Leu Gly			

480	485	490	495	
gtg att gaa gac cac tcg aat cga aca cgt ctt gct aaa ctt ctt agg				1714
Val Ile Glu Asp His Ser Asn Arg Thr Arg Leu Ala Lys Leu Leu Arg				
	500	505	510	
ttc cag tct tct cat cat cca act gac att act agc cta gac cag tat				1762
Phe Gln Ser Ser His His Pro Thr Asp Ile Thr Ser Leu Asp Gln Tyr				
	515	520	525	
gtg gaa aga atg aag gaa aaa caa gac aaa atc tac ttc atg gct ggg				1810
Val Glu Arg Met Lys Glu Lys Gln Asp Lys Ile Tyr Phe Met Ala Gly				
	530	535	540	
tcc agc aga aaa gag gct gaa tct tct cca ttt gtt gag cga ctt ctg				1858
Ser Ser Arg Lys Glu Ala Glu Ser Ser Pro Phe Val Glu Arg Leu Leu				
	545	550	555	
aaa aag ggc tat gaa gtt att tac ctc aca gaa cct gtg gat gaa tac				1906
Lys Lys Gly Tyr Glu Val Ile Tyr Leu Thr Glu Pro Val Asp Glu Tyr				
	560	565	570	575
tgt att cag gcc ctt ccc gaa ttt gat ggg aag agg ttc cag aat gtt				1954
Cys Ile Gln Ala Leu Pro Glu Phe Asp Gly Lys Arg Phe Gln Asn Val				
	580	585	590	
gcc aag gaa gga gtg aag ttc gat gaa agt gag aaa act aag gag agt				2002
Ala Lys Glu Gly Val Lys Phe Asp Glu Ser Glu Lys Thr Lys Glu Ser				
	595	600	605	
cgt gaa gca gtt gag aaa gaa ttt gag cct ctg ctg aat tgg atg aaa				2050
Arg Glu Ala Val Glu Lys Glu Phe Glu Pro Leu Leu Asn Trp Met Lys				
	610	615	620	
gat aaa gcc ctt aag gac aag att gaa aag gct gtg gtg tct cag cgc				2098
Asp Lys Ala Leu Lys Asp Lys Ile Glu Lys Ala Val Val Ser Gln Arg				
	625	630	635	
ctg aca gaa tct ccg tgt gct ttg gtg gcc agc cag tac gga tgg tct				2146
Leu Thr Glu Ser Pro Cys Ala Leu Val Ala Ser Gln Tyr Gly Trp Ser				
	640	645	650	655
ggc aac atg gag aga atc atg aaa gca caa gcg tac caa acg ggc aag				2194
Gly Asn Met Glu Arg Ile Met Lys Ala Gln Ala Tyr Gln Thr Gly Lys				
	660	665	670	
gac atc tct aca aat tac tat gcg agt cag aag aaa aca ttt gaa att				2242
Asp Ile Ser Thr Asn Tyr Tyr Ala Ser Gln Lys Lys Thr Phe Glu Ile				
	675	680	685	
aat ccc aga cac ccg ctg atc aga gac atg ctt cga cga att aag gaa				2290
Asn Pro Arg His Pro Leu Ile Arg Asp Met Leu Arg Arg Ile Lys Glu				
	690	695	700	
gat gaa gat gat aaa aca gtt ttg gat ctt gct gtg gtt ttg ttt gaa				2338
Asp Glu Asp Asp Lys Thr Val Leu Asp Leu Ala Val Val Leu Phe Glu				
	705	710	715	
aca gca acg ctt ccg tca ggg tat ctt tta cca gac act aaa gca tat				2386
Thr Ala Thr Leu Arg Ser Gly Tyr Leu Leu Pro Asp Thr Lys Ala Tyr				
	720	725	730	735
gga gat aga ata gaa aga atg ctt cgc ctc agt ttg aac att gac cct				2434
Gly Asp Arg Ile Glu Arg Met Leu Arg Leu Ser Leu Asn Ile Asp Pro				

740	745	750	
gat gca aag gtg gaa gaa gag cct gaa gaa gaa cct gaa gag aca gca			2482
Asp Ala Lys Val Glu Glu Glu Pro Glu Glu Glu Pro Glu Glu Thr Ala			
755	760	765	
gaa gac aca aca gaa gac aca gag caa gac gaa gat gaa gaa atg gat			2530
Glu Asp Thr Thr Glu Asp Thr Glu Gln Asp Glu Asp Glu Glu Met Asp			
770	775	780	
gtg gga aca gat gaa gaa gaa gaa aca gca aag gaa tct aca gct gaa			2578
Val Gly Thr Asp Glu Glu Glu Glu Thr Ala Lys Glu Ser Thr Ala Glu			
785	790	795	
aaa gat gaa ttg taa attatactct caccatttgg atcctgtgtg gagagggaat			2633
Lys Asp Glu Leu *			
800			
gtgaaattta catcatttct ttttgggaga gacttgtttt ggatgcccc taatccccctt			2693
ctccccctgca ctgtaaaatg tgggattatg ggtcacagga aaaagtgggt tttttagttg			2753
aattttttttt aacatttctc atgaatgtaa atttgtacta ttttaactgac tattcttgat			2813
gtaaaatctt gtcattgtga taaaaataaa aaagatccca aat			2856

<210> 4
 <211> 415
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(249)

<400> 4			
ttg cgg aat tcg gca cga ggc cga cta caa cag att gga gcc atg gct			48
Leu Arg Asn Ser Ala Arg Gly Arg Leu Gln Gln Ile Gly Ala Met Ala			
1 5 10 15			
ttg gaa cag aac cag tca aca gat tat tat tat gag gaa aat gaa atg			96
Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn Glu Met			
20 25 30			
aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc aaa gaa			144
Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile Lys Glu			
35 40 45			
gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc aca ata			192
Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu Thr Ile			
50 55 60			
gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca att tat			240
Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala Ile Tyr			
65 70 75 80			
gcc aaa cat taaaata tctcgacccc taaaagttct gctcacagtc gttatagttt			296
Ala Lys His			
tcattgtcac tcaactgcct tataacattg tcaagttctg ccgagccata gacatcatct			356

actccctgat caccagctgc aacatgagca aacgcatgga catcgccatc caagtcaca 415

<210> 5
 <211> 3190
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (653)..(1072)

<400> 5
 tccttgaccg gtccggaatt cccgggtcga cgatttcgtg gcggtagctg ctttccccac 60
 aaacccaaac tacatcccca aggtcagggc caggctctgt tgagtaatgc tccccatcac 120
 agcacgcagc acaaggctgg ctgtttgaca aatacacaca taaccaaag acatgtgaat 180
 gtggtttccc aactcacttt aaacaaatat tccgggacca acttcaagga cgttctacaa 240
 cagaaactgg actgtactct tcacaaacat caatgtcatg aaagacagaa aggctgagga 300
 cctgtctcaa acgaaaggag gctgcagaga ggacaactaa aggcagcgtt tgatcctgga 360
 ttggatcctg gaccagaaaa acaacggctt tcaaatcat tattgggaca gttggcaaat 420
 ttgaaacagg aactacaaat tagcaactcc tgggctgata agagaatatt acacatttcc 480
 tgaatttgag aactgtacca tgggcatgtg agaggctgtc cctgttcttg ggaaatgttc 540
 actaaaacat cttacggata aacgagcatg atgtatacaa ataactctca aatggttcat 600
 gggtcagaga ggataggaag aaacaggggt gagggagaag aggaggggaac ga atg 655
 Met
 1
 aaa gag aaa atg tgg caa aat gtt ctt tgt tgt acc ctt caa act gct 703
 Lys Glu Lys Met Trp Gln Asn Val Leu Cys Cys Thr Leu Gln Thr Ala
 5 10 15
 gtg att ttg aaa tta ttt caa aat aaa gtt tta aat att tta aaa aat 751
 Val Ile Leu Lys Leu Phe Gln Asn Lys Val Leu Asn Ile Leu Lys Asn
 20 25 30
 ttt ttt ctt tct ccc ctt gat acc agg aag aat aaa gtt ttt aaa aaa 799
 Phe Phe Leu Ser Pro Leu Asp Thr Arg Lys Asn Lys Val Phe Lys Lys
 35 40 45
 tgg gca ggt ggg cca ggc gcg gtg gct cac gcc tgt aat ccc agc act 847
 Trp Ala Gly Gly Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr
 50 55 60 65
 ttg gga ggc cga ggc ggg cgg atc aca aag tca gga gat cga gac cat 895
 Leu Gly Gly Arg Gly Gly Arg Ile Thr Lys Ser Gly Asp Arg Asp His
 70 75 80
 cct ggc caa cac ggt gaa acc cgg tct cta cta aaa gta caa aaa att 943
 Pro Gly Gln His Gly Glu Thr Arg Ser Leu Leu Lys Val Gln Lys Ile
 85 90 95

agc cag gtg tgg tgg cag atg act gta ggc caa gct aat tgg gag gct	991
Ser Gln Val Trp Trp Gln Met Thr Val Gly Gln Ala Asn Trp Glu Ala	
100 105 110	
 gag gca gga gaa tgg tgc gaa ccc ggg gag ggc aga gct tgc agt gag	1039
Glu Ala Gly Glu Trp Cys Glu Pro Gly Glu Gly Arg Ala Cys Ser Glu	
115 120 125	
 cca aga tca ccc act gca ctc cag act ggg taa cagagcaa gactcggctc	1090
Pro Arg Ser Pro Thr Ala Leu Gln Thr Gly *	
130 135 140	
 caaaaaaaaaat aataagttac atttaaattgt catatacata tttaagaaaa aaaaaaccaa	1150
gtacttctca tttaagacag agtagaaatt atttaaaatt aggagttggg gtaaaggatg	1210
agctacatat tcaagtcaaa ttatagtaag tattcactat tccactacca aagtaggtca	1270
attatactaa agagaagaaa tctatgtgaa ttgaggcatt ttctcacttt gatatatgtg	1330
aataaatttc aggttgtcta aattcctagg gttatatagt tagaaatata taattctctt	1390
atagacaggt caactagggg aaataagtta gcacaatcat ttgaattggg tgtctacata	1450
ctgggcaggg cttattcctt ttcttttagct tctttgcaca tgtaaagcag gccataagat	1510
gtcctgtttt gccatggaca atgcaacat ttttaggtcg accttgacaa atcacacaag	1570
gttcaatggc attaaggggc aaactagatt ccacactctc ttctttgtct tgggtttctt	1630
ccctttcaaa ctctttcaca tcttcttggc tgcataaat aatgctacta gaagttgatg	1690
gctgagaata gtcttcactt tcttgtgatt gtgaagcttg tgtaatttta tcatcatttt	1750
cctcaacaca tgactctctg gaatcattca ctatagtttt tttaacaatca ggaacatcaa	1810
agccctcttc agcttgtgtt gagttttcca gtttggtctt ctgagagatt tcccccttat	1870
ctttcccttt atcttcagga agccaattct cacgaagggc ccaacatctg ttgcaatgtg	1930
atggaagggg gggattcatt tcattgcatg aagtgcattt ccaatagtca gctaaggaaa	1990
tttcaggatc ttcttcaaat gaatctgtat cactctcccc tgcttgatac acagtaactt	2050
gatatactc atcatcttca tctgagagtt cttgtccttc ttcactaagg ctataatctt	2110
ctgagtcgag agattcaact tcaaattcta cactaaactg atctgaaact gaatcctgat	2170
ccaaccaatc acctgaatgt tcacttacac cagcatcaag atccggattc gatggcgtcc	2230
ctgtagattc actgctactg cttctttcac aacatatctc ccttattaca cacagagcca	2290
ggctttcatc aaaggaaagg gaaatactat cagatttgtg gcgttttctt tgtcgttcac	2350
cagataattc atctgaattt tcttctgtct cactaattgc tctccttcta gatgaggtag	2410
atgggtctaga aaccaaattg gaagatgaag gtttctcttc ctgaagctct tgtacaagggt	2470
ccttttgatc actccacct tcaagggtgac acctgttctc actcacagat gtacctgagt	2530
ccgatgattc ctgctgattg actactacca agttcctgta gatcatggta tatattttcc	2590
tgtgctcttt cacagagaag ctgggcacgc caaacaatc tcctagaaga tcatttgaac	2650

aatatacaat atgttggtgc ttctcatcat ataatcgttt agtcataata tactggccaa 2710
 gataaaaaag aacctctttc atagtataag tgtctttttg tgcaccaaca gactttaata 2770
 acttcaaaag caatggctttt ggtctaacca ggggtctcttg ttccgaagct ggaatctgtg 2830
 aggtgggttac agcaccatca gtaggtacag acatgttggt attgcacatt tgcctgctcc 2890
 tcaccatccg gggttttcgc gcttggagtc ggggggccct caagactccc cagtttcctt 2950
 cacggggact gactactgcg gaagcacgac gccctggggc tcggggatca ttccactctc 3010
 cgggccaggg cactggggcg tcgtacgcac taatccgggg agggacgggtg ctctggtg 3070
 cgaaagcagc aggatctcgg tcagaggggt cgcggccgcc cctcgggctc ggcttcttgc 3130
 tccatctttc cgacacacag ggccacacag gccccagaag cagccaagct cgcgcggtgc 3190

<210> 6
 <211> 1343
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (291) .. (1109)

<400> 6
 gcggccgccc cggcggtcc tggaaccccg gttcgcggcg atgccagcca cccagcgaa 60
 gccgcgcgag ttcagtgtt ggataatttg aaagtacaat agttggtttc cctgtccacc 120
 cgccccactt cgcttgccat cacagcacgc ctatcggatg tgagaggaga agtcccgctg 180
 ctcgggcact gtctatatac gcctaacacc tacatatatt ttaaaaaacat taaatataat 240
 taacaatcaa aagaaagagg agaaaggaag ggaagcatta ctgggttact atg cac 296
 Met His
 1
 ttg cga ctg att tot tgg ctt ttt atc att ttg aac ttt atg gaa tac 344
 Leu Arg Leu Ile Ser Trp Leu Phe Ile Ile Leu Asn Phe Met Glu Tyr
 5 10 15
 atc ggc agc caa aac gcc tcc cgg gga agg cgc cag cga aga atg cat 392
 Ile Gly Ser Gln Asn Ala Ser Arg Gly Arg Arg Gln Arg Arg Met His
 20 25 30
 cct aac gtt agt caa ggc tgc caa gga ggc tgt gca aca tgc tca gat 440
 Pro Asn Val Ser Gln Gly Cys Gln Gly Gly Cys Ala Thr Cys Ser Asp
 35 40 45 50
 tac aat gga tgt ttg tca tgt aag ccc aga cta ttt ttt gct ctg gaa 488
 Tyr Asn Gly Cys Leu Ser Cys Lys Pro Arg Leu Phe Phe Ala Leu Glu
 55 60 65
 aga att ggc atg aag cag att gga gta tgt ctc tct tca tgt cca agt 536
 Arg Ile Gly Met Lys Gln Ile Gly Val Cys Leu Ser Ser Cys Pro Ser
 70 75 80
 gga tat tat gga act cga tat cca gat ata aat aag tgt aca aaa tgc 584

Gly	Tyr	Tyr	Gly	Thr	Arg	Tyr	Pro	Asp	Ile	Asn	Lys	Cys	Thr	Lys	Cys	
85							90					95				
aaa gct gac tgt gat acc tgt ttc aac aaa aat ttc tgc aca aaa tgt																632
Lys Ala Asp Cys Asp Thr Cys Phe Asn Lys Asn Phe Cys Thr Lys Cys																
100							105					110				
aaa agt gga ttt tac tta cac ctt gga aag tgc ctt gac aat tgc cca																680
Lys Ser Gly Phe Tyr Leu His Leu Gly Lys Cys Leu Asp Asn Cys Pro																
115					120					125					130	
gaa ggg ttg gaa gcc aac aac cat act atg gag tgt gtc agt att gtg																728
Glu Gly Leu Glu Ala Asn Asn His Thr Met Glu Cys Val Ser Ile Val																
				135					140					145		
cac tgt gag gtc agt gaa tgg aat cct tgg agt cca tgc acg aag aag																776
His Cys Glu Val Ser Glu Trp Asn Pro Trp Ser Pro Cys Thr Lys Lys																
				150				155						160		
gga aaa aca tgt ggc ttc aaa aga ggg act gaa aca cgg gtc cga gaa																824
Gly Lys Thr Cys Gly Phe Lys Arg Gly Thr Glu Thr Arg Val Arg Glu																
				165			170					175				
ata ata cag cat cct tca gca aag ggt aac cta tgt ccc cca aca aat																872
Ile Ile Gln His Pro Ser Ala Lys Gly Asn Leu Cys Pro Pro Thr Asn																
				180			185					190				
gag aca aga aag tgt aca gtg caa agg aag aag tgt cag aag gga gaa																920
Glu Thr Arg Lys Cys Thr Val Gln Arg Lys Lys Cys Gln Lys Gly Glu																
195					200				205						210	
cga gga aaa aaa gga agg gag agg aaa aga aaa aaa cct aat aaa gga																968
Arg Gly Lys Lys Gly Arg Glu Arg Lys Arg Lys Lys Pro Asn Lys Gly																
				215				220						225		
gaa agt aaa gaa gca ata cct gac agc aaa agt ctg gaa tcc agc aaa																1016
Glu Ser Lys Glu Ala Ile Pro Asp Ser Lys Ser Leu Glu Ser Ser Lys																
				230				235						240		
gaa atc cca gag caa cga gaa aac aaa cag cag cag aag aag cga aaa																1064
Glu Ile Pro Glu Gln Arg Glu Asn Lys Gln Gln Gln Lys Lys Arg Lys																
				245				250						255		
gtc caa gat aaa cag aaa tcg gta tca gtc agc act gta cac tag agg																1112
Val Gln Asp Lys Gln Lys Ser Val Ser Val Ser Thr Val His *																
				260				265						270		
gttccatgag attattgtag actcatgatg ctgctatctc aaccagatgc ccaggacagg																1172
tgctctagcc attaggacca caaatggaca tgtcagttat tgctctgtct aaacaacatt																1232
cccagtagtt gctatattct tcatacaagc atagttaaca acaaagagcc aaaagatcaa																1292
agaagggata ctttcagatg gttgtcttgt gtgcttctct gcatttttaa a																1343

<210> 7
 <211> 973
 <212> DNA
 <213> Homo sapiens
 <220>

<221> CDS

<222> (1)..(795)

<400> 7

atg gat cca acc atc tca acc ttg gac aca gaa ctg aca cca atc aac	48
Met Asp Pro Thr Ile Ser Thr Leu Asp Thr Glu Leu Thr Pro Ile Asn	
1 5 10 15	
gga act gag gag act ctt tgc tac aag cag acc ttg agc ctc acg gtg	96
Gly Thr Glu Glu Thr Leu Cys Tyr Lys Gln Thr Leu Ser Leu Thr Val	
20 25 30	
ctg acg tgc atc gtt tcc ctt gtc ggg ctg aca gga aac gca gtt gtg	144
Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val	
35 40 45	
ctc tgg ctc ctg ggc tgc cgc atg cgc agg aac gcc ttc tcc atc tac	192
Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr	
50 55 60	
atc ctc aac ttg gcc gca gca gac ttc ctc ttc ctc agc ggc cgc ctt	240
Ile Leu Asn Leu Ala Ala Asp Phe Leu Phe Leu Ser Gly Arg Leu	
65 70 75 80	
ata tat tcc ctg tta agc ttc atc agt atc ccc cat acc atc tct aaa	288
Ile Tyr Ser Leu Leu Ser Phe Ile Ser Ile Pro His Thr Ile Ser Lys	
85 90 95	
atc ctc tat cct gtg atg atg ttt tcc tac ttt gca ggc ctg agc atg	336
Ile Leu Tyr Pro Val Met Met Phe Ser Tyr Phe Ala Gly Leu Ser Met	
100 105 110	
ctg agc acc atc agc acc gag cac cgc ctg tcc gtc ctg tgg ccc atc	384
Leu Ser Thr Ile Ser Thr Glu His Arg Leu Ser Val Leu Trp Pro Ile	
115 120 125	
tgg tac tgc tgc cac tgc ccc aca cac ctg tca gcg gtc atg tgt gtc	432
Trp Tyr Cys Cys His Cys Pro Thr His Leu Ser Ala Val Met Cys Val	
130 135 140	
ctg ctc tgg gcc ctg tcc ctg ttg cag agc atc ctg gag tgg atg ttc	480
Leu Leu Trp Ala Leu Ser Leu Leu Gln Ser Ile Leu Glu Trp Met Phe	
145 150 155 160	
tgt agc ttc ctg ttt agt gat gtt gac tct gat aat tgg tgt caa ata	528
Cys Ser Phe Leu Phe Ser Asp Val Asp Ser Asp Asn Trp Cys Gln Ile	
165 170 175	
tta gat ttc ctc aca gtc gcg tgg ctg att ttt tta atc tgt ggt tct	576
Leu Asp Phe Leu Thr Val Ala Trp Leu Ile Phe Leu Ile Cys Gly Ser	
180 185 190	
ctg tgg gtt cac cct ggt cct gct gat cag gat cat atg tgg atc ccg	624
Leu Trp Val His Pro Gly Pro Ala Asp Gln Asp His Met Trp Ile Pro	
195 200 205	
gaa gat acc gct gac cag gct gta tgt gac cat cct gct cac agg gct	672
Glu Asp Thr Ala Asp Gln Ala Val Cys Asp His Pro Ala His Arg Ala	
210 215 220	
ggt ctt cct cct ctg tgg cct gcc cct cag cat tca gtt ttt cct att	720
Gly Leu Pro Pro Leu Trp Pro Ala Pro Gln His Ser Val Phe Pro Ile	
225 230 235 240	

ata ctg gat cca cgt gga cag gga agt ctt att ttg tca tgt tca tct 768
 Ile Leu Asp Pro Arg Gly Gln Gly Ser Leu Ile Leu Ser Cys Ser Ser
 245 250 255
 agt ttc tat ttt cct gtc cgc tct taa cagca gtgccaaccc catcatttac 820
 Ser Phe Tyr Phe Pro Val Arg Ser *
 260 265
 ttcttcgtgg gctccttttag gcagcgtcaa aataggcaga acctgaagct gggttctccag 880
 agggctctgc aggacgcgtc tgaggtggat gaaggtggag ggcagcttcc tgaggaaatc 940
 ctggagctgt cgggaagcag attggagcag tga 973

<210> 8
 <211> 639
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (217) .. (453)

<400> 8
 atttgccct cgaggccaag aattcggcac gaggcgcttt tgcaaagccg cggaggtgaa 60
 gtgaacttag aggttggtggg gccgaggggt cgtcttatag ctaccagccc acaggcattt 120
 agtctacgtt ggaggtaaac aaatacgggt cctgcttagg agaaaagaaa aacgtcttac 180
 agccagtgtc taaactccaa acaacggaat gtatca atg aga cct tgt ata tgg 234
 Met Arg Pro Cys Ile Trp
 1 5
 ata cac gtg cat tta aaa ccg ccc tgc cgg ctt gta gag ctt ttg ccg 282
 Ile His Val His Leu Lys Pro Pro Cys Arg Leu Val Glu Leu Leu Pro
 10 15 20
 ttc tcc agc gct tta cag ggg tta tgc cac tta agc ctc gga aca act 330
 Phe Ser Ser Ala Leu Gln Gly Leu Ser His Leu Ser Leu Gly Thr Thr
 25 30 35
 tta cca gtg att cta cca gaa agg aat gaa gaa cag aac ctt cag gaa 378
 Leu Pro Val Ile Leu Pro Glu Arg Asn Glu Glu Gln Asn Leu Gln Glu
 40 45 50
 ttg agt cac aat gca gac aaa tat caa atg gga gat tgt tgc aag gaa 426
 Leu Ser His Asn Ala Asp Lys Tyr Gln Met Gly Asp Cys Cys Lys Glu
 55 60 65 70
 gag att gat gat agt att ttc tac tag ccatt gggaagataa aaggagacag 478
 Glu Ile Asp Asp Ser Ile Phe Tyr *
 75
 aagattgaag cctttgccag ccattctttc cctttttgct tccaaactcc tcaactggga 538
 accttcatat gtgcagtatt tatattggat catactgggtg attataaaag ttcctaggag 598
 gctagaagag ccaaccaaca gagaagggaa agcagctctgt t 639

<210> 9
 <211> 3522
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (416) .. (2353)

<220>
 <221> misc_feature
 <222> (1) ... (3522)
 <223> n = a,t,c or g

<400> 9
 ccgagccgag cgccgaggac cgtgctaccc caggcccggg ctgcccagc gcaggctcct 60
 ctctggcagc agcggcggcg cggngacccc ngtcctcgg cctccnnttc ccateccacc 120
 tcccgagcct tcctcttccc gcagcacgcc cggcccggcc cggccgtggc cctcctcagt 180
 gccggccgc c atggcagagg cgtccggcgc ggggaaaatc tagcccgggg atttcatgcg 240
 gcctagctcg gttccgcctc ctctcgcgc ggcaccagcg gctgcccga cccagcccc 300
 actccgggcc tccgtgtctc tcctgtgatc gcaactgacac ggccgggggg ttagaatgga 360
 aaaaactgaa ggcccgatga gagaaaggga aagttaagga tgctggagca gaaca atg 418
 Met
 1
 gat ttc tct ttc tct ttc atg caa ggg atc atg gga aac aca att cag 466
 Asp Phe Ser Phe Ser Phe Met Gln Gly Ile Met Gly Asn Thr Ile Gln
 5 10 15
 caa cca cct caa ctc att gac tcc gcc aac atc cgt cag gag gat gcc 514
 Gln Pro Pro Gln Leu Ile Asp Ser Ala Asn Ile Arg Gln Glu Asp Ala
 20 25 30
 ttt gat aac aac agt gac att gct gaa gat ggt ggc cag aca cca tat 562
 Phe Asp Asn Asn Ser Asp Ile Ala Glu Asp Gly Gly Gln Thr Pro Tyr
 35 40 45
 gaa gct act ttg cag caa ggc ttt cag tac cca gct aca aca gaa gat 610
 Glu Ala Thr Leu Gln Gln Gly Phe Gln Tyr Pro Ala Thr Thr Glu Asp
 50 55 60 65
 ctt cct cca ctc aca aat ggg tat cca tca tca atc agt gtg tat gaa 658
 Leu Pro Pro Leu Thr Asn Gly Tyr Pro Ser Ser Ile Ser Val Tyr Glu
 70 75 80
 act caa acc aaa tac cag tca tat aat cag tat cct aat ggg tca gcc 706
 Thr Gln Thr Lys Tyr Gln Ser Tyr Asn Gln Tyr Pro Asn Gly Ser Ala
 85 90 95
 aat ggc ttt ggt gca gtt aga aac ttt agc ccc act gac tat tat cat 754
 Asn Gly Phe Gly Ala Val Arg Asn Phe Ser Pro Thr Asp Tyr Tyr His
 100 105 110
 tca gaa att cca aac aca aga cca cat gaa att ctg gaa aaa cct tcc 802
 Ser Glu Ile Pro Asn Thr Arg Pro His Glu Ile Leu Glu Lys Pro Ser
 115 120 125

cct cca cag cca cca cct cct cct tcg gta cca caa act gtg att cca	850
Pro Pro Gln Pro Pro Pro Pro Ser Val Pro Gln Thr Val Ile Pro	
130 135 140 145	
aag aag act ggc tca cct gaa att aaa cta aaa ata acc aaa act atc	898
Lys Lys Thr Gly Ser Pro Glu Ile Lys Leu Lys Ile Thr Lys Thr Ile	
150 155 160	
cag aat ggc agg gaa ttg ttt gag tct tcc ctt tgt gga gac ctt tta	946
Gln Asn Gly Arg Glu Leu Phe Glu Ser Ser Leu Cys Gly Asp Leu Leu	
165 170 175	
aat gaa gta cag gca agt gag cac acg aaa tca aag cat gaa agc aga	994
Asn Glu Val Gln Ala Ser Glu His Thr Lys Ser Lys His Glu Ser Arg	
180 185 190	
aaa gaa aag agg aaa aaa agc aac aag cat gac tca tca aga tct gaa	1042
Lys Glu Lys Arg Lys Lys Ser Asn Lys His Asp Ser Ser Arg Ser Glu	
195 200 205	
gag cgc aag tca cac aaa atc ccc aaa tta gaa cca gag gaa caa aat	1090
Glu Arg Lys Ser His Lys Ile Pro Lys Leu Glu Pro Glu Glu Gln Asn	
210 215 220 225	
aga cca aat gag agg gtt gac act gta tca gaa aaa cca agg gaa gaa	1138
Arg Pro Asn Glu Arg Val Asp Thr Val Ser Glu Lys Pro Arg Glu Glu	
230 235 240	
cca gta cta aaa gag gaa gcc cca gtt cag cca ata cta tct tct gtt	1186
Pro Val Leu Lys Glu Glu Ala Pro Val Gln Pro Ile Leu Ser Ser Val	
245 250 255	
cca aca acg gaa gtg tcc act ggt gtt aag ttt cag gtt ggc gat ctt	1234
Pro Thr Thr Glu Val Ser Thr Gly Val Lys Phe Gln Val Gly Asp Leu	
260 265 270	
gtg tgg tcc aag gtg gga acc tat cct tgg tgg cct tgt atg gtt tca	1282
Val Trp Ser Lys Val Gly Thr Tyr Pro Trp Trp Pro Cys Met Val Ser	
275 280 285	
agt gat ccc cag ctt gag gtt cat act aaa att aac aca aga ggt gcc	1330
Ser Asp Pro Gln Leu Glu Val His Thr Lys Ile Asn Thr Arg Gly Ala	
290 295 300 305	
cga gaa tat cat gtc cag ttt ttt agc aac cag cca gag agg gcg tgg	1378
Arg Glu Tyr His Val Gln Phe Phe Ser Asn Gln Pro Glu Arg Ala Trp	
310 315 320	
gtt cat gaa aaa cgg gta cga gag tat aaa ggt cat aaa cag tat gaa	1426
Val His Glu Lys Arg Val Arg Glu Tyr Lys Gly His Lys Gln Tyr Glu	
325 330 335	
gaa tta ctg gct gag gca acc aaa caa gcc agc aat cac tct gag aaa	1474
Glu Leu Leu Ala Glu Ala Thr Lys Gln Ala Ser Asn His Ser Glu Lys	
340 345 350	
caa aag att cgg aaa ccc cga cct cag aga gaa cgt gct cag tgg gat	1522
Gln Lys Ile Arg Lys Pro Arg Pro Gln Arg Glu Arg Ala Gln Trp Asp	
355 360 365	
att ggc att gcc cat gca gag aaa gca ttg aaa atg act cga gaa gaa	1570
Ile Gly Ile Ala His Ala Glu Lys Ala Leu Lys Met Thr Arg Glu Glu	
370 375 380 385	

aga ata gaa cag tat act ttt att tac att gat aaa cag cct gaa gag	1618
Arg Ile Glu Gln Tyr Thr Phe Ile Tyr Ile Asp Lys Gln Pro Glu Glu	
390 395 400	
gct tta tcc caa gca aaa aag agt gtt gcc tcc aaa acc gaa gtt aaa	1666
Ala Leu Ser Gln Ala Lys Lys Ser Val Ala Ser Lys Thr Glu Val Lys	
405 410 415	
aaa acc cga cga cca aga tct gtg ctg aat act cag cca gaa cag acc	1714
Lys Thr Arg Arg Pro Arg Ser Val Leu Asn Thr Gln Pro Glu Gln Thr	
420 425 430	
aat gca ggg gag gtg gcc tcc tca ctc tca agt act gaa att cgg aga	1762
Asn Ala Gly Glu Val Ala Ser Ser Leu Ser Ser Thr Glu Ile Arg Arg	
435 440 445	
cat agc cag agg cgg cac aca agt gcg gaa gag gaa gag cca ccg cct	1810
His Ser Gln Arg Arg His Thr Ser Ala Glu Glu Glu Glu Pro Pro Pro	
450 455 460 465	
gtt aaa ata gcc tgg aaa act gcg gca gca agg aaa tcc tta cca gct	1858
Val Lys ,Ile Ala Trp Lys Thr Ala Ala Ala Arg Lys Ser Leu Pro Ala	
470 475 480	
tcc att acg atg cac aaa ggg agc ctg gat ttg cag aag tgt aac atg	1906
Ser Ile Thr Met His Lys Gly Ser Leu Asp Leu Gln Lys Cys Asn Met	
485 490 495	
tct cca gtt gtg aaa att gaa caa gtg ttt gct ctt cag aat gct aca	1954
Ser Pro Val Val Lys Ile Glu Gln Val Phe Ala Leu Gln Asn Ala Thr	
500 505 510	
ggg gat ggg aaa ttt atc gat caa ttt gtt tat tca aca aag gga att	2002
Gly Asp Gly Lys Phe Ile Asp Gln Phe Val Tyr Ser Thr Lys Gly Ile	
515 520 525	
ggt aac aaa aca gaa ata agt gtc agg ggg caa gac agg ctt ata att	2050
Gly Asn Lys Thr Glu Ile Ser Val Arg Gly Gln Asp Arg Leu Ile Ile	
530 535 540 545	
tct aca cca aac cag aga aat gaa aag cca acg cag agt gta tca tct	2098
Ser Thr Pro Asn Gln Arg Asn Glu Lys Pro Thr Gln Ser Val Ser Ser	
550 555 560	
cct gaa gca aca tct ggt tct aca ggc tca gta gaa aag aag caa cag	2146
Pro Glu Ala Thr Ser Gly Ser Thr Gly Ser Val Glu Lys Lys Gln Gln	
565 570 575	
aga aga tca att aga act cgt tct gaa tca gag aaa tcc act gag gtt	2194
Arg Arg Ser Ile Arg Thr Arg Ser Glu Ser Glu Lys Ser Thr Glu Val	
580 585 590	
gtg cca aag aag aag atc aaa aag gag cag gtt gaa aca gtt cct cag	2242
Val Pro Lys Lys Lys Ile Lys Lys Glu Gln Val Glu Thr Val Pro Gln	
595 600 605	
gct aca gtg aag act gga tta cag aaa ggg tcc gcg gac cgg gga gtg	2290
Ala Thr Val Lys Thr Gly Leu Gln Lys Gly Ser Ala Asp Arg Gly Val	
610 615 620 625	
cag ggc tct gtc aga ttc agt gac agc tcc gtc tcc gca gcg att gag	2338
Gln Gly Ser Val Arg Phe Ser Asp Ser Ser Val Ser Ala Ala Ile Glu	
630 635 640	

gaa act gtg gac tga gattcctgta caatttcac cagaaaactc cagacttgta 2393
 Glu Thr Val Asp *
 645
 gtctccatgc aagatttctt tgcggcggc ttgataaaca gtttctttgt ttctgatttt 2453
 gatttcgcca atcatcatta ttggcatttt cctgcctggg ttcttcttca agactctgaa 2513
 caattgcttt aacagtcaaa tgattttttt ttttcgggtt gagctggatg ggtacagctt 2573
 aaatcatggg tccagcctaa aaaccacat ttaacttaca ctgatcaatt tcaacatgga 2633
 ctgttttttg ttttttggtt ttaaataaag catcattaat gcacatctgc aggggtttgc 2693
 caaacagccc aaactgtata cattacaatc attaaaagtt cttatttttt ttaatatagg 2753
 tgccgttatc atggagaaca gcatgacagc tgtctttggc agtctgtcat ttttctagca 2813
 ttttcagaaa ctcatcgga atggcggtac ctgtgtttcc cttcgaaagc ctctcagtac 2873
 agcactcctg ttctctgtt aaaactcctt gttaatccag tgatctttta ggccaaggaa 2933
 atattttgtg atgggtgttct ggggtccatac accagcaatg aaggagatag atttgtgtac 2993
 ttgtgttttt taatcagcat taacatgggc aggcaccctc atttatagat gtcaggaaac 3053
 attcagtga aaactttag aatgggatgt gataacgagg ttccagtaat ctgagcagtc 3113
 taacgaggcc cacctcctcc accacagaac gtggctatgt tccaagtgt actctcactc 3173
 agcctgttgc ggatcttcat ggcctcagga gacttggttc tccatgggct cttctggact 3233
 gcacacttcc accatagctt gctgggttga tctagatgtc tgtttgttgt atggaaattt 3293
 tgggggaaaa aatccaaaac acaaactgtg ggttgaaata ttaaccgtct ccttggttcc 3353
 ttggtattca ccgtgcctga tctgcacatt tcatcggtggc tgtttctgta tagcctatac 3413
 tgcattagcc caagagattg ttgctttgta actttttgca ctattgtttt ggctggattt 3473
 gtattacaca cagtttttaa aaaaacaatt ccacactaaa aaaaaaaaaa 3522

<210> 10
 <211> 2366
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (174) .. (1541)

<400> 10
 cctcagcctc cccgcgcgcg ccgcgcgcgc cgcgcgcgag ccggtttctt ttttccggcg 60
 ctccgggtgc gagagacagg tcgggcccc taggcagcga gccgcagcgc aatcccggcg 120
 ctgcgccaa gaccctggaa gctaccgtta cccgcgcggg cagcgtgggc gcc atg 176
 Met
 1

agc agc tcg gga ctg aat tcg gag aag gta gct gct ctg ata cag aaa	224
Ser Ser Ser Gly Leu Asn Ser Glu Lys Val Ala Ala Leu Ile Gln Lys	
5 10 15	
ctg aat tcc gac ccc cag ttc gta ctt gcc cag aat gtc ggg acc acc	272
Leu Asn Ser Asp Pro Gln Phe Val Leu Ala Gln Asn Val Gly Thr Thr	
20 25 30	
cac gac ctg ctg gac atc tgt ctg aag cgg gcc acg gtg cag cgc gcg	320
His Asp Leu Leu Asp Ile Cys Leu Lys Arg Ala Thr Val Gln Arg Ala	
35 40 45	
cag cat gtg ttc cag cac gcc gtg ccc cag gag ggc aag cca atc acc	368
Gln His Val Phe Gln His Ala Val Pro Gln Glu Gly Lys Pro Ile Thr	
50 55 60 65	
aac cag aag agc tca ggg cga tgc tgg atc ttt tct tgt ctg aat gtt	416
Asn Gln Lys Ser Ser Gly Arg Cys Trp Ile Phe Ser Cys Leu Asn Val	
70 75 80	
atg agg ctt cca ttc atg aaa aag tta aat att gaa gaa ttt gag ttt	464
Met Arg Leu Pro Phe Met Lys Lys Leu Asn Ile Glu Glu Phe Glu Phe	
85 90 95	
agc caa tct tac ctg ttt ttt tgg gac aag gtt gaa cgc tgt tat ttc	512
Ser Gln Ser Tyr Leu Phe Phe Trp Asp Lys Val Glu Arg Cys Tyr Phe	
100 105 110	
ttc ttg agt gct ttt gtg gac aca gcc cag aga aag gag cct gag gat	560
Phe Leu Ser Ala Phe Val Asp Thr Ala Gln Arg Lys Glu Pro Glu Asp	
115 120 125	
ggg agg ctg gtg cag ttt ttg ctt atg aac cct gca aat gat ggt ggc	608
Gly Arg Leu Val Gln Phe Leu Leu Met Asn Pro Ala Asn Asp Gly Gly	
130 135 140 145	
caa tgg gat atg ctt gtt aat att gtt gaa aaa tat ggt gtt atc cct	656
Gln Trp Asp Met Leu Val Asn Ile Val Glu Lys Tyr Gly Val Ile Pro	
150 155 160	
aag aaa tgc ttc cct gaa tct tat aca aca gag gca acc aga agg atg	704
Lys Lys Cys Phe Pro Glu Ser Tyr Thr Thr Glu Ala Thr Arg Arg Met	
165 170 175	
aat gat att ctg aat cac aag atg aga gaa ttc tgt ata cga ctg cgg	752
Asn Asp Ile Leu Asn His Lys Met Arg Glu Phe Cys Ile Arg Leu Arg	
180 185 190	
aac ctg gta cac agt gga gca acc aaa gga gaa atc tcg gcc aca cag	800
Asn Leu Val His Ser Gly Ala Thr Lys Gly Glu Ile Ser Ala Thr Gln	
195 200 205	
gac gtc atg atg gag gag ata ttc cga gtg gtg tgc atc tgt ttg ggt	848
Asp Val Met Met Glu Glu Ile Phe Arg Val Val Cys Ile Cys Leu Gly	
210 215 220 225	
aat cca cca gag aca ttc acc tgg gaa tat cga gac aaa gat aaa aat	896
Asn Pro Pro Glu Thr Phe Thr Trp Glu Tyr Arg Asp Lys Asp Lys Asn	
230 235 240	
tat cag aaa att ggc ccc ata aca ccc ttg gag ttt tac agg gaa cat	944
Tyr Gln Lys Ile Gly Pro Ile Thr Pro Leu Glu Phe Tyr Arg Glu His	
245 250 255	

gtc aag cca ctc ttc aat atg gaa gat aag att tgt tta gtg aat gac	992
Val Lys Pro Leu Phe Asn Met Glu Asp Lys Ile Cys Leu Val Asn Asp	
260 265 270	
cct agg ccc cag cac aag tac aac aaa ctt tac aca gtg gaa tac tta	1040
Pro Arg Pro Gln His Lys Tyr Asn Lys Leu Tyr Thr Val Glu Tyr Leu	
275 280 285	
agc aat atg gtt gga ggg aga aaa act cta tac aac aac cag ccc att	1088
Ser Asn Met Val Gly Gly Arg Lys Thr Leu Tyr Asn Asn Gln Pro Ile	
290 295 300 305	
gac ttc ctg aaa aag atg gtt gct gcc tcc atc aaa gat gga gag gct	1136
Asp Phe Leu Lys Lys Met Val Ala Ala Ser Ile Lys Asp Gly Glu Ala	
310 315 320	
gtg tgg ttt ggc tgt gat gtt gga aaa cac ttc aat agc aag ctg ggc	1184
Val Trp Phe Gly Cys Asp Val Gly Lys His Phe Asn Ser Lys Leu Gly	
325 330 335	
ctc agt gac atg aat ctc tat gac cat gag tta gtg ttt ggt gtc tcc	1232
Leu Ser Asp Met Asn Leu Tyr Asp His Glu Leu Val Phe Gly Val Ser	
340 345 350	
ttg aag aac atg aat aaa gcg gag agg ctg act ttt ggt gag tca ctt	1280
Leu Lys Asn Met Asn Lys Ala Glu Arg Leu Thr Phe Gly Glu Ser Leu	
355 360 365	
atg acc cac gcc atg acc ttc act gct gtc tca gag aag gat gat cag	1328
Met Thr His Ala Met Thr Phe Thr Ala Val Ser Glu Lys Asp Asp Gln	
370 375 380 385	
gat ggt gct ttc aca aaa tgg aga gtg gag aat tca tgg ggt gaa gac	1376
Asp Gly Ala Phe Thr Lys Trp Arg Val Glu Asn Ser Trp Gly Glu Asp	
390 395 400	
cat ggc cac aaa ggt tac ctg tgc atg aca gat gag tgg ttc tct gag	1424
His Gly His Lys Gly Tyr Leu Cys Met Thr Asp Glu Trp Phe Ser Glu	
405 410 415	
tat gtc tac gaa gtg gtg gtg gac agg aag cat gtc cct gaa gag gtg	1472
Tyr Val Tyr Glu Val Val Val Asp Arg Lys His Val Pro Glu Glu Val	
420 425 430	
cta gct gtg tta gag cag gaa ccc att atc ctg cca gca tgg gac ccc	1520
Leu Ala Val Leu Glu Gln Glu Pro Ile Ile Leu Pro Ala Trp Asp Pro	
435 440 445	
atg gga gct ttg gct gag tga ta ctgccctcca gctctttcct ccttccatgg	1573
Met Gly Ala Leu Ala Glu *	
450 455	
aaactgacgt agctgcaaag gacagatcca gggactgaag ccaaagttat gcaagggact	1633
gtgtgttgcc acaggacaca gtcagatttc cagtctccac caggaacctc ttcagaaagt	1693
gtgctttatg ctgaaacaga atactgttaa aggaaaaaaaa agagggggga agatcaggtc	1753
atactatcta ctctcctcat ctctaacagc tcaggatctc ttagcatttt aattagatgt	1813
aattgtttgt ctttaactgt caaaaagttt ggttctgtgt ctgtgtttta ataagacgag	1873
aggacgagcg attgaggtgt atggagagaa aacagaccta atgctccttg ttcctagagt	1933

```

agagtggagg gaggggtggcc taagagttga gctctcggaa ctgcatgctg ctggacagta 1993
tcactgtctt tcctagatgg cagtcactga attccatttt ttcaaggtaa tttcttgtgc 2053
ctctaatagc ccaagaatgg gaggttgatc agatctgaca tgattccttc ctgttctgaa 2113
ctgtgggggtg cacatctctg cttgagtcag gtttgagtag aggcttagag acagttgggt 2173
gagaacaacc aaaatcttat catggtctca gtcataatca ttagggggaa ctctagccaa 2233
atggtttaac ttctgcctgt ggaactgggg attgggtggg caggaaaagg tgatatccat 2293
tctttctgat aactagatgg tgctgagaag cttttgaata aaaactttgc taaatgagaa 2353
taagctgaaa aaa 2366

```

```

<210> 11
<211> 1732
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (241)..(495)

```

```

<400> 11
gatgcctgat ctcatcaatc tagcgggaga gacaggataa cctgtccgag agtatagcgc 60
cacttatgac tccgccggaa aaattacttt aaaaatcgcc aaaaattact tggagcaaag 120
ggcagtcagg cggcgttcgc caaggtggcg cagtcggttt tgacctgtag cagagaacca 180
attctggaga acagcctcac ttctttgatt gaatacttac ataatgcatt ggaacatgac 240
atg aga tta agg ttt aat aat gat aga atg aag acc aca ata aaa gag 288
Met Arg Leu Arg Phe Asn Asn Asp Arg Met Lys Thr Thr Ile Lys Glu
1 5 10 15
acc aca atc ctt agc tca gca att ctt acc ttt ctt acc tat ttg atg 336
Thr Thr Ile Leu Ser Ser Ala Ile Leu Thr Phe Leu Thr Tyr Leu Met
20 25 30
aag atg tct ttt gaa agg tgt act gca agg aac aaa atg ttt gta aat 384
Lys Met Ser Phe Glu Arg Cys Thr Ala Arg Asn Lys Met Phe Val Asn
35 40 45
tct ccc ttt tac cca agg gtg gat aat tac tgt acc tcc tca tgg aaa 432
Ser Pro Phe Tyr Pro Arg Val Asp Asn Tyr Cys Thr Ser Ser Trp Lys
50 55 60
aag ttt tat tta aag tgt tat ttc tca ttg aat act atc aaa aag gaa 480
Lys Phe Tyr Leu Lys Cys Tyr Phe Ser Leu Asn Thr Ile Lys Lys Glu
65 70 75 80
aaa aaa atg acc taa acttttgaga tagatttggc tctagtaagt atttagttat 535
Lys Lys Met Thr *
85
atcacttgca tatctgggag aagaaataag agactatcat cagtacattc ccatctacta 595
aaaaaattta ttttacacat gtcaagggat tacttataac ttccatttta ttactaatag 655

```

```

cttgaaccct tttaatgaag acctaactcc tccaccagaa atttaagttt atgttcttac    715
tttgtttact tataaaatac atctcaggta tttcggatgt cttttttttt tctaagccta    775
tatgaaatga aaaatatatt ggcaaagtaa atgtttaaac cttttacgtt aaaattactt    835
tgaaagatga aaagtttagtg ctgtttttgt cacgttatac tgaaaattaaa tgtttataat    895
ttatattttg ggtttatgta taaatcatgg aatttatgca aaaatatgag tagtacagat    955
tctcctctaa ttctgtagga ctttgaataa tgtgatattt ttcttataat tggacccttg   1015
tgttttgaag aaatgccaac tgcttgaaga atctccttgt tatttgtatt atttgctata   1075
gggttagatg ttgagaaatt ctgctgacaa aaaattttta gccagtttta cactaaatgt   1135
tcctcagtct gattaatttg ttattggatg tattctgtat ctttcttttg taatttgtaa   1195
cttttatcca cttagcacga atgattctat taaagaaaat cattaggaag tggtagaaac   1255
tttaaactgc ccagagttt gcctgtttcc atattttatt atcttataat cttcgggagt   1315
gcttacactt atggagctaa cattttcaga gatacagctt cttatagtaa cactaaaact   1375
ttcttctctt ttggactgaa tacctataat tataactata tggtagttta agtttccttg   1435
tgattagtca aaaataccat tttagtatga agcaatgaag tctattatth gttgtcccat   1495
aattgagaaa gcttaaatac accttttatt aagagtthgt aaattctagc ttagtctaca   1555
cagattttta tatcaatttg tttatatttt tattaatgtc atttctggaa gtgtgaaaat   1615
gttaatgttc aacaagcaac attaaaaata gatttgaaac atttatatat agagaggtag   1675
acatttatth actgtttagg tactgaagat tatcacttaa taaaaaatat atatccc    1732

```

```

<210> 12
<211> 2913
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (511) .. (2913)

```

```

<400> 12
atgaatatgg acatcaatga ttggtacttc gctactcatc atggtgatat tagcggttct    60
agacatatcc tggatttggg actactaaaa gcgcaaaaga aggcccagag aaggagcac    120
atgctaaaac ttgaggctga gaagaaaaag cttcgaacta tacttcaagt tcagtatgta    180
ttgcagaact tgacacagga gcacgtacaa aaagacttca aaggggggtt gaatggtgca    240
gtgtatttgc cttcaaaaga acttgactac ctcatthaagt tttcaaaact gacctgccct    300
gaaagaaatg aaagtctgag tgttgaagac cagatggagc agtcacctt gtacttttgg    360
gaccttttgg aaggtagtga gaaagcagtg gtaggaacga catacaaaca cttgaaggat    420

```